

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 22:17:11 ; Search time 30.4828 Seconds

(Without alignments)
4385.960 Million cell updates/sec

Title: US-09-983-025B-2

Perfect score: 9856
Sequence: 1 MMCKIIRISLAIAGWALC.....AADCDLDECTCRDKAEHQ 1791

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/1aa/5A_COMB.pep: *
2: /cgn2_6/ptodata/1/1aa/5B_COMB.pep: *
3: /cgn2_6/ptodata/1/1aa/6A_COMB.pep: *
4: /cgn2_6/ptodata/1/1aa/6B_COMB.pep: *
5: /cgn2_6/ptodata/1/1aa/PTCUS_COMB.pep: *
6: /cgn2_6/ptodata/1/1aa/backfilest.pep: *

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	9836	99.8	1791	4	US-09-827-998-3
2	9507	96.5	1770	4	US-09-827-998-10
3	7363	74.7	1385	4	US-09-827-998-16
4	1709	17.3	717	4	US-09-949-016-9436
5	336.5	3.4	3594	4	US-09-911-842A-4
6	330.5	3.0	3571	4	US-09-911-842A-2
7	292.5	2.9	2489	4	US-09-911-842A-5
8	287.5	2.9	1847	6	5256642-10
9	287.5	2.9	1847	6	5472939-10
10	287.5	2.9	1847	6	5256642-10
11	287.5	2.9	1847	6	5472939-10
12	287.5	2.9	2039	6	5256642-2
13	287.5	2.9	2039	6	5472939-2
14	287.5	2.9	2039	6	5256642-2
15	287.5	2.9	2039	6	5472939-2
16	287	2.9	1947	4	US-09-612-314A-52
17	283	2.9	1466	6	5256642-6
18	283	2.9	1466	6	5472939-6
19	283	2.9	1466	6	5256642-6
20	283	2.9	1466	6	5472939-6
21	283	2.9	1537	6	5256642-5
22	283	2.9	1537	6	5472939-5
23	283	2.9	1537	6	5256642-5
24	283	2.9	1537	6	5472939-5
25	253.5	2.6	849	4	US-09-949-016-10271
26	249	2.5	830	1	US-08-110-158-4
27	249	2.5	1033	4	US-09-834-309-1

28	243.5	2.5	830	5	PCT-US91-05059-2
29	236	2.4	577	2	US-08-435-149-3
30	236	2.4	611	3	US-09-475-460A-32
31	236	2.4	611	4	US-09-748-061A-32
32	235.5	2.4	574	6	5378464-3
33	235.5	2.4	574	6	5378464-3
34	235	2.4	630	6	5378464-2
35	235	2.4	830	6	5378464-2
36	230.5	2.3	610	1	US-08-365-470-3
37	230.5	2.3	610	3	US-09-209-668-19
38	230.5	2.3	610	3	US-09-009-490A-89
39	230.5	2.3	610	4	US-09-949-016-5942
40	230.5	2.3	610	6	5217870-2
41	230.5	2.3	610	6	5217870-2
42	230.5	2.3	647	4	US-09-949-016-10272
43	225	2.3	1394	4	US-09-949-016-5971
44	225	2.3	1394	6	5177197-30
45	225	2.3	1394	6	5177197-30

ALIGNMENTS

```
RESULT 1
US-09-827-998-3
Sequence 3, Application US/09827998
Patent No. 6656700
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OR INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDIMORF-8
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Neomica Sequence Listing Engine
Patent No. 6656700
SEQ ID NO 3
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-998-3
Query Match 99.8%; Score 9836; DB 4; Length 1791;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1788; Conservative 1; Mismatches 2; Indels 0; Gaps 0;
QY 1 MMCKIIRISLAIAGWALCSANSELGWTTRKSLVERHNLQVLLBGRGWLGAQRPR 60
DB 1 MMCKIIRISLAIAGWALCSANSELGWTTRKSLVERHNLQVLLBGRGWLGAQRPR 60
QY 61 ASPQHILFGVYPSAAGNYLRPYVGEQRIHTHTGSKPTTEGNASLVLPDITENPAGIRG 120
DB 61 ASPQHILFGVYPSAAGNYLRPYVGEQRIHTHTGSKPTTEGNASLVLPDITENPAGIRG 120
QY 121 AVEBPAPPMWGDSPITGSELGDDAVILGNORSKESIGEGAGIOKGSMAAATTTTIAIFTTL 180
DB 121 AVEBPAPPMWGDSPITGSELGDDAVILGNORSKESIGEGAGIOKGSMAAATTTTIAIFTTL 180
QY 181 NEPPETORRGWAKSRORQVWKRRADGQDSGISHPQWPHSLKRRVKSPPBESN 240
DB 181 NEPPETORRGWAKSRORQVWKRRADGQDSGISHPQWPHSLKRRVKSPPBESN 240
QY 241 ONGEGSYREARETFNSQVGLPILYFGRRERLLRPVLAETPREAFTVEAMVVRPEGQN 300
DB 241 ONGEGSYREARETFNSQVGLPILYFGRRERLLRPVLAETPREAFTVEAMVVRPEGQN 300
QY 301 NPATIAVPNDCKSTVSDKGMALGIRSGKDKGRDARFPFSLCTDRYKATILISHSRVQ 360
DB 301 NPATIAVPNDCKSTVSDKGMALGIRSGKDKGRDARFPFSLCTDRYKATILISHSRVQ 360
```

301 NPATIAAGVFNDCSHTVSDKGMALGIRSGDKRKDARPPFSLCTDRVKKATILISHSRXQ 360
QY 361 PGMTTHAATYDGERHMLYVDTGTVASSLDOSGPLNSPMMASCSLSLLIGSSSBDGHR 420
Db 361 PGYTHAATYDGERHMLYVDTGTVASSLDOSGPLNSPMMASCSLSLLIGSSSBDGHR 420
QY 421 GHLGTLVWMTALPOSHFOHSSOHSSGGEAEATDLVLTASFPPVNTWMPFDEKXPRL 480
Db 421 GHLGTLVWMTALPOSHFOHSSOHSSGGEAEATDLVLTASFPPVNTWMPFDEKXPRL 480
QY 481 LQGEPEBEILSPIOPLCQGTVCNDELISQYNGWPLRGEKXIRYOVVNICDEGLNP 540
Db 481 LQGEPEBEILSPIOPLCQGTVCNDELISQYNGWPLRGEKXIRYOVVNICDEGLNP 540
QY 541 IVSEEOIRLOHEALNEAFSRYNISWQLSVHQVHNSLHRVVLVNCESKIGNDHCDEC 600
Db 541 IVSEEOIRLOHEALNEAFSRYNISWQLSVHQVHNSLHRVVLVNCESKIGNDHCDEC 600
QY 601 EHPITGXDGCRCRQGRCSWNRBDGLCHECNMNLNFDGDCDDPOVADVRKTCFDPD 660
Db 601 EHPITGXDGCRCRQGRCSWNRBDGLCHECNMNLNFDGDCDDPOVADVRKTCFDPD 660
QY 661 SPKRAYSVKELKALQLNSTHPLNIYYPASSVRBDLAGAATWMDKAVTHLGGIVLSPA 720
Db 661 SPKRAYSVKELKALQLNSTHPLNIYYPASSVRBDLAGAATWMDKAVTHLGGIVLSPA 720
QY 721 YYGMPGHTDMIHVGHVGLGYHYVFKGYSERESCNDCPKETVPSEMGDLCAADTAPPKS 780
Db 721 YYGMPGHTDMIHVGHVGLGYHYVFKGYSERESCNDCPKETVPSEMGDLCAADTAPPKS 780
QY 781 ELCEPEPTSTCGFTFRPGAPFTNYSYTDNCTDNFTPNQVARMHCYLDLVYQOMTES 840
Db 781 ELCEPEPTSTCGFTFRPGAPFTNYSYTDNCTDNFTPNQVARMHCYLDLVYQOMTES 840
QY 841 RKPTPIPIPMVIGQTNKSLTIHMLPRISGVVYDASGLCGACTEDGTFRQYVHTASR 900
Db 841 RKPTPIPIPMVIGQTNKSLTIHMLPRISGVVYDASGLCGACTEDGTFRQYVHTASR 900
QY 901 RVCCSSGWTPEEAVGPVDVQCEPSLOAMSPEVHLVHMNTVPCPEGGSLELFPHP 960
Db 901 RVCCSSGWTPEEAVGPVDVQCEPSLOAMSPEVHLVHMNTVPCPEGGSLELFPHP 960
QY 961 VQADTLTLMTVSFMESSQVLFDEIILENKESVHLGDLDFCDIPLTIKLVHDKVSGV 1020
Db 961 VQADTLTLMTVSFMESSQVLFDEIILENKESVHLGDLDFCDIPLTIKLVHDKVSGV 1020
QY 1021 KVTYFDERIEIDALLTSQPHSLCSGCRPVRYQVLRDPPASGLPVVVTSHRKFDTVE 1080
Db 1021 KVTYFDERIEIDALLTSQPHSLCSGCRPVRYQVLRDPPASGLPVVVTSHRKFDTVE 1080
QY 1081 VTPBOMVOYVLAAGGELGASAPLNIHGAPOGDKVEBRIGEBDDGDIYSGDGS 1140
Db 1081 VTPBOMVOYVLAAGGELGASAPLNIHGAPOGDKVEBRIGEBDDGDIYSGDGS 1140
QY 1141 KVCLEBEGFNCVGEPSLCYMEGDCICERFERKTSIYVCGIYTPKGYLDQMATRAYSHE 1200
Db 1141 KVCLEBEGFNCVGEPSLCYMEGDCICERFERKTSIYVCGIYTPKGYLDQMATRAYSHE 1200
QY 1201 DKKKCPVSLVTGBPHSLICTSYHPLPMHRLTGMPFCVASENETDODRSBQPEGLKE 1260
Db 1201 DKKKCPVSLVTGBPHSLICTSYHPLPMHRLTGMPFCVASENETDODRSBQPEGLKE 1260
QY 1261 DEWVLKVCENRPGARAFIFLITDGLVPRGEHOPTVLYLTVDRGSHSGTYGLSQOH 1320
Db 1261 DEWVLKVCENRPGARAFIFLITDGLVPRGEHOPTVLYLTVDRGSHSGTYGLSQOH 1320
QY 1321 NPLIINTVTHONVLFHHTTSVILNFSAPRIGISAVALTSTRIGLSAPSNCISEDEGONH 1380
Db 1321 NPLIINTVTHONVLFHHTTSVILNFSAPRIGISAVALTSTRIGLSAPSNCISEDEGONH 1380
QY 1381 QGSGCIRHPCGKODSCPSLLIDHADVVNCTSIGPLMKCAITCORGFALQASSGQYIRPM 1440
Db 1381 QGSGCIRHPCGKODSCPSLLIDHADVVNCTSIGPLMKCAITCORGFALQASSGQYIRPM 1440

QY 1441 QKEILLTCSGSHMDONVSCLPVDCGVPDPSLVNRYANFSCSEGTFLKRCGISICVPAKQ 1500
Db 1441 QKEILLTCSGSHMDONVSCLPVDCGVPDPSLVNRYANFSCSEGTFLKRCGISICVPAKQ 1500
QY 1501 GLSPMLTCLBEGDLSLEBYVCKLECDAPPIILNANLLPHCLQDNHVGTTCKYECKRGY 1560
Db 1501 GLSPMLTCLBEGDLSLEBYVCKLECDAPPIILNANLLPHCLQDNHVGTTCKYECKRGY 1560
QY 1561 YVASAAGKRNKLLKIQCLEBGITWEGSCIPVYCEPPPPVFEEMVETCTNGFSLDSCVL 1620
Db 1561 YVASAAGKRNKLLKIQCLEBGITWEGSCIPVYCEPPPPVFEEMVETCTNGFSLDSCVL 1620
QY 1621 NCONERKPLICTKEGLMTQEPFLCENLQCECPPEPSSELSVEYKCEOGYIGAVCSPL 1680
Db 1621 NCONERKPLICTKEGLMTQEPFLCENLQCECPPEPSSELSVEYKCEOGYIGAVCSPL 1680
QY 1681 CVIPSPDPMVLPENITADTLEHMMEPYKQISVCTGRQWHPDVLVHCIOSCPFAQDG 1740
Db 1681 CVIPSPDPMVLPENITADTLEHMMEPYKQISVCTGRQWHPDVLVHCIOSCPFAQDG 1740
QY 1741 WCDTINNRAYCHYDGDGSCSSTLSSKVIIPPAACDIDECTCRDPAKEBNQ 1791
Db 1741 WCDTINNRAYCHYDGDGSCSSTLSSKVIIPPAACDIDECTCRDPAKEBNQ 1791

RESULT 2
US-09-827-998-10
; Sequence 10, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDMPORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 10
; LENGTH: 1770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-10

Query Match 96.5%; Score 9507; DB 4; Length 1770;
Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;
Matches 1732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MMCLIKIRISIALIAGMALCSANSELGWTBKSLIVEREHLNOVLLBGERCMLGAKVRRP 60
Db 1 MMCLIKIRISIALIAGMALCSANSELGWTBKSLIVEREHLNOVLLBGERCMLGAKVRRP 60
QY 61 ASPQHLLFGVYPSRAGNYLAPRYVGEBOEIIHTGSKSKDTBGANAVSLVPPDLTENPAGLRG 120
Db 61 ASPQHLLFGVYPSRAGNYLAPRYVGEBOEIIHTGSKSKDTBGANAVSLVPPDLTENPAGLRG 120
QY 121 AVEBPAPWVGDSYIGSELLGDDDAYLGNORSKESIGEGAIQSGSMAAATTTAIFTL 180
Db 121 AVEBPAPWVGDSYIGSELLGDDDAYLGNORSKESIGEGAIQSGSMAAATTTAIFTL 180
QY 181 NEPPETQRGMAKSRORQVWKRAEDGOGDSGISSHFQWPWPKSLKHYKXSPPEESN 240
Db 181 NEPPETQRGMAKSRORQVWKRAEDGOGDSGISSHFQWPWPKSLKHYKXSPPEESN 240
QY 241 QNGEGSYREAEFTNSQVGLPIILYFSGRRELLLRPEVLAIEIPREAFTEAMVVRBEGON 300
Db 241 QNGEGSYREAEFTNSQVGLPIILYFSGRRELLLRPEVLAIEIPREAFTEAMVVRBEGON 300

```

QY 301 NPATIAGVNDGCSHTVSDKGWALGIRSGKDKKDPARFFPSLCTDRVKKATITILSHSHYQ 360
Db 301 NPATIAGVNDGCSHTVSDKGWALGIRSGKDKKDPARFFPSLCTDRVKKATITILSHSHYQ 360
QY 361 PGTWTHVAATYDGRHMLYVDGTQVASSLDOSGPLNSPFMASCSRLILGDSSEBGFYR 420
Db 361 PGTWTHVAATYDGRHMLYVDGTQVASSLDOSGPLNSPFMASCSRLILGDSSEBGFYR 420
QY 421 GHLGTLVFWSTALPQSHFQSHSQQSHSGEEBATDLVLTNSFEPVTEWVPFDEKXPRLV 480
Db 421 GHLGTLVFWSTALPQSHFQSHSQQSHSGEEBATDLVLTNSFEPVTEWVPFDEKXPRLV 480
QY 481 LQGEPEPELISPLQPLCGQTCVCDNVLLISQYNGWYPLRGEKYLRYVAVNICDEGLNP 540
Db 481 LQGEPEPELISPLQPLCGQTCVCDNVLLISQYNGWYPLRGEKYLRYVAVNICDEGLNP 540
QY 541 IVSEEOIRLQHEALNEAFSRYNISWQLSVHQVNSTLRHRYVLVNCBPSKIGNDHCDEPC 600
Db 541 IVSEEOIRLQHEALNEAFSRYNISWQLSVHQVNSTLRHRYVLVNCBPSKIGNDHCDEPC 600
QY 601 EHPPLTYDGDGCRILQGRCYSWNRDGLCHVECNMNLNFDGDCDDPQVADVRKTCFDPD 660
Db 601 EHPPLTYDGDGCRILQGRCYSWNRDGLCHVECNMNLNFDGDCDDPQVADVRKTCFDPD 660
QY 661 SPKRAVMSVKELKALQUNSTHPLNTIYFASVREDLAGAATWPMKDAVTHLGGIVLSPA 720
Db 661 SPKRAVMSVKELKALQUNSTHPLNTIYFASVREDLAGAATWPMKDAVTHLGGIVLSPA 720
QY 721 YYGNGHTDITMIEHGVHGLGYHVPKGVSEESCNCPCKETVPSMETGDLCAADTAPRKS 780
Db 721 YYGNGHTDITMIEHGVHGLGYHVPKGVSEESCNCPCKETVPSMETGDLCAADTAPRKS 780
QY 781 ELCEPEPTSDTCGTRPFGAPFTNYMSYTDNCTDNFTNPQVAMHCYLDLVYQWTES 840
Db 781 ELCEPEPTSDTCGTRPFGAPFTNYMSYTDNCTDNFTNPQVAMHCYLDLVYQWTES 840
QY 841 RKPRPIRPPWVIGOTNKSLLTIHMLPRISGVYDRASSSLGACCEDETFQYVHTASSR 900
Db 841 RKPRPIRPPWVIGOTNKSLLTIHMLPRISGVYDRASSSLGACCEDETFQYVHTASSR 900
QY 901 RVCDSSGWTPEBEAVGPDPVQPCPSLQANSPEVHLVHMMNTVPCPTGEGSLLELFOHP 960
Db 901 RVCDSSGWTPEBEAVGPDPVQPCPSLQANSPEVHLVHMMNTVPCPTGEGSLLELFOHP 960
QY 961 VQADTLTLMWTSFPMESQVLPDTEILLENKESVHLGDLTFCDIPLTIKLVADKVS 1020
Db 961 VQADTLTLMWTSFPMESQVLPDTEILLENKESVHLGDLTFCDIPLTIKLVADKVS 1020
QY 1021 KVTFFDERIEIDALLTSQHPSPICSGCRPVRYQVLRPPRASGLPVVYVTHSHKFTDVE 1080
Db 1021 KVTFFDERIEIDALLTSQHPSPICSGCRPVRYQVLRPPRASGLPVVYVTHSHKFTDVE 1080
QY 1081 VTPGOMYQVLAEGELGASPPNLNIGHAPYCGDDKVSBRLEGECDDDDLVSGDGS 1140
Db 1081 VTPGOMYQVLAEGELGASPPNLNIGHAPYCGDDKVSBRLEGECDDDDLVSGDGS 1140
QY 1141 KVCLEBEGFNCVGEPSLCTYMEGDGICBPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200
Db 1141 KVCLEBEGFNCVGEPSLCTYMEGDGICBPFERKTSIVDCGIYTPKGYLDQWATRAYSSHE 1200
QY 1201 DKKCCPVSLVGEHSLICTSYHNDLPNHRPLTGWFPVASENETODDRSQPBGSLKKE 1260
Db 1201 DKKCCPVSLVGEHSLICTSYHNDLPNHRPLTGWFPVASENETODDRSQPBGSLKKE 1260
QY 1261 DEWMLKVCFNRPGEARAFIFLITTDGLVPGHQPVTVLITVDRGSHSLGTTGLSGQH 1320
Db 1261 DEWMLKVCFNRPGEARAFIFLITTDGLVPGHQPVTVLITVDRGSHSLGTTGLSGQH 1320
QY 1321 NPLIINTVTHQNVLPFHHTSVLNFSSPRVGISAVALTSSRIGLSAPSNCSIBDEGQNH 1380
Db 1321 NPLIINTVTHQNVLPFHHTSVLNFSSPRVGISAVALTSSRIGLSAPSNCSIBDEGQNH 1380

```

```

QY 1381 QGSCIRHPCGKODSCPSLLLDHADVNVCTSIGPLMKCAITTCORGFALQASSGQYIRPM 1440
Db 1381 QGSCIRHPCGKODSCPSLLLDHADVNVCTSIGPLMKCAITTCORGFALQASSGQYIRPM 1440
QY 1441 QKEILLTCSGSHQDQVNSCLPVDGCVDPSPSLVANYANFSGSEGTFLKRCGISCVPPAKLQ 1500
Db 1441 QKEILLTCSGSHQDQVNSCLPVDGCVDPSPSLVANYANFSGSEGTFLKRCGISCVPPAKLQ 1500
QY 1501 GLSPMLTCLBGLMSLBEVYKLECDAPRILNANLLPHCLQNHVDGTICKECKRGY 1560
Db 1501 GLSPMLTCLBGLMSLBEVYKLECDAPRILNANLLPHCLQNHVDGTICKECKRGY 1560
QY 1561 YVASAEGKVNKLKIQCEGGEIWEQSCIPVCEPPPFVEGVECTNGFSLDSQCVL 1620
Db 1561 YVASAEGKVNKLKIQCEGGEIWEQSCIPVCEPPPFVEGVECTNGFSLDSQCVL 1620
QY 1621 NCONREKPLILCTKEGLMTQEFKLCENTQCECPPEPSELNSVBKCEQYIGAVCSPL 1680
Db 1621 NCONREKPLILCTKEGLMTQEFKLCENTQCECPPEPSELNSVBKCEQYIGAVCSPL 1680
QY 1681 CVTPSPDPVMLPENITADTLEHMMBPVKVQSVICTGRQMHDPVLYVHCIOQCE 1734
Db 1681 CVTPSPDPVMLPENITADTLEHMMBPVKVQSVICTGRQMHDPVLYVHCIOQCE 1734

RESULT 3
US-09-9827-998-16
; Sequence 16, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MIMORE-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 16
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-9827-998-16

Query Match 74.7%; Score 7363; DB 4; Length 1385;
Best Local Similarity 77.0%; Pred. No. 0;
Matches 1379; Conservative 0; Mismatches 6; Indels 406; Gaps 1;

```

QY	301	NPALIIAGVFDNCSHTVSDKGMAALGIRSGKDKKRDAREFFBSLCTDRVKKATITLISHSRQ	360
Db	301	NPALIIA-----	306
QY	361	PGTWTHTAATYDGRMALVYDQTVASSLIDGCLNDFPMASCRSLILGGPSSBDGHYR	420
Db	307	-----	306
QY	421	GHLGTLVFWSTALPQSHQSHSSQSHSGBEATDVLVTASFEFVNTWVPFRDEKXPRLVEV	480
Db	307	-----	306
QY	481	LOGFEPPEIILSPLOPPLCGQTVCDNVELISQYNGYMWPLRGEKXIRYQVANI CDDEGLNP	540
Db	307	-----	306
QY	541	IVSEBQILQHBEALNEAFSRNYSWQSLVHQYHNSTLHRVVLVNCPSRSKIGNDHCDDEC	600
Db	307	-----	306
QY	601	EHPILGYDGDORLQGRCYSMWRNRDGLCHEBCNNMLNDFDDGCCDPQVADVTKTCFDPD	660
Db	307	-----	306
QY	661	SPKRAYMSVKELKEALQLNSTHPLNIYFASSVREDLAGAATWPMWDXAVTHLGGIVLSPA	720
Db	307	-----GGIVLSPA	314
QY	721	YYGMPGHDTMIHEVGHVLGLYHVPKGVSRBSCNDPCKEYVPSMEGDLCAQDAPRYSKS	780
Db	315	YYGMPGHDTMIHEVGHVLGLYHVPKGVSRBSCNDPCKEYVPSMETGDLCAQDAPRYSKS	374
QY	781	ELCREPEPSTDCCGFTRPGAFPTMYMSYTNDCTDNFTPNQVAMHCYLDLVYQOMTES	840
Db	375	ELCREPEPSTDCCGFTRPGAFPTMYMSYTNDCTDNFTPNQVAMHCYLDLVYQOMTES	434
QY	841	RKPTPIPIPEMWIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEDGTFRQYHTASSR	900
Db	435	RKPTPIPIPEMWIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEDGTFRQYHTASSR	494
QY	901	RVCSSGGTWPEBEANPRPDVOPCEBSLQAMSPENHLYHMMYVPCPRGSGLELPHOP	960
Db	495	RVCSSGGTWPEBEANPRPDVOPCEBSLQAMSPENHLYHMMYVPCPRGSGLELPHOP	554
QY	961	VOADTILTLMTVSYFMESQOVLFDTEIILLENKESVHALGLDFFCDIPLTIKLHVDGKXSGV	1020
Db	555	VOADTILTLMTVSYFMESQOVLFDTEIILLENKESVHALGLDFFCDIPLTIKLHVDGKXSGV	614
QY	1021	KVYTFDERIEIDAALLITSQPHSPILCSGCRPVRYQVLRDPFPAAGLPUVVVTHSHRKFTDVE	1080
Db	615	KVYTFDERIEIDAALLITSQPHSPILCSGCRPVRYQVLRDPFPAAGLPUVVVTHSHRKFTDVE	674
QY	1081	VTPQGMVYQVLAENGELGELGASAPPLNHIHGAPYGGDGKVSBRUGCECDGDLVSGDCCS	1140
Db	675	VTPQGMVYQVLAENGELGELGASAPPLNHIHGAPYGGDGKVSBRUGCECDGDLVSGDCCS	734
QY	1141	KVCLEBEBFNCVGBERSLCYMTEGDCICEPFRKRTSYVDCGYTTPKGYLDQWATRAYSHE	1200
Db	735	KVCLEBEBFNCVGBERSLCYMTEGDCICEPFRKRTSYVDCGYTTPKGYLDQWATRAYSHE	794
QY	1201	DKKKCPVSLVYGEPSHSLICTSYHPDLPHNRPLTWGFPVCVASENETODDRSBQPSGLKXE	1260
Db	795	DKKKCPVSLVYGEPSHSLICTSYHPDLPHNRPLTWGFPVCVASENETODDRSBQPSGLKXE	854
QY	1261	DEWMLKVCFNRPGEARAFIFILPTDGLVPGHQOPTVTLIYTLTVDRGSHSIGTYGLSCQH	1320
Db	855	DEWMLKVCFNRPGEARAFIFILPTDGLVPGHQOPTVTLIYTLTVDRGSHSIGTYGLSCQH	914
QY	1321	NPLIINTVHHONVLFPHHTSYVLNPSRVSAGVSAVALTSSRIGLSAPNSNCISBDEGQNH	1380
Db	915	NPLIINTVHHONVLFPHHTSYVLNPSRVSAGVSAVALTSSRIGLSAPNSNCISBDEGQNH	974
QY	1381	QGOSCIHRPCCOKODSCPSILLDLHDADVNVCTSIGBPLMKCATTCORGFALQASSGQYIRPM	1440

Db	975	QGGSCIHRRPCKODSCBSLBDHADVANCISIGGLMKCATTCQGRFPLQASSSEQYITLM	103
Qy	1441	QKEIILLTSSGSHMDQVNSCLPVDGVPDPISLVNYANFSCSEGTFLKRCGISICVPAPKIQ	1500
Db	1035	QKEIILLTSSGSHMDQVNSCLPVDGVPDPISLVNYANFSCSEGTFLKRCGISICVPAPKIQ	1094
Qy	1501	GLSPMLTCLLEGMLSLPEVYCKLECDAPITLIANNLILPHCLQDNHDVGTICKECKRGY	1566
Db	1095	GLSPMLTCLLEGMLSLPEVYCKLECDAPITLIANNLILPHCLQDNHDVGTICKECKRGY	1154
Qy	1561	YVAESABEKVANKLILKIQCLEGGIMWQSGCIPVVCBPPPVYFEGMEYECTNGFSLDSQVL	1620
Db	1155	YVAESABEKVANKLILKIQCLEGGIMWQSGCIPVVCBPPPVYFEGMEYECTNGFSLDSQVL	1214
Qy	1621	NCNDBREKTLPLCTCKEGLMTQEFKLCENLQSECBPPPSBELNSVYKCEQYIGIGAVCSPL	1680
Db	1215	NCNDBREKTLPLCTCKEGLMTQEFKLCENLQSECBPPPSBELNSVYKCEQYIGIGAVCSPL	1274
Qy	1681	CVIPSPDPVMLPENITADTLEHNMPEPVQVGSIVCTGRGRQHPDPVLVHICQSCBEPFQADG	1740
Db	1275	CVIPSPDPVMLPENITADTLEHNMPEPVQVGSIVCTGRGRQHPDPVLVHICQSCBEPFQADG	1334
Qy	1741	WCDTINNRAYCHYDGGDCSSSTLSSKKVYIPAPADCDLDECTGRDPKAEENO	1791
Db	1335	WCDTINNRAYCHYDGGDCSSSTLSSKKVYIPAPADCDLDECTGRDPKAEENO	1385

```

RESULT 4
US-09-949-016-9436
; Sequence 9436, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CLO01307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO. 9436
; LENGTH: 717
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-9436

```

	Query Match	17.3%	Score 1709;	DB 4;	Length 717;
	Best Local Similarity	43.0%	Pred. No. 1.7e-119;		
	Matches 310;	Conservative 140;	Mismatches 237;	Indels 34;	Gaps 14;
Qy	1084 GOMTQYVLMAGELGELGEASPLNHLINGAPYCGDGKYSERLGEBCDDGLVSDGCSKVC				
	1143				
Db	6 GSYVQYWMVITISGTRESEBSPDAVTVIHSGSYCGDGIITQKDQGEQCDMMNKINGGCSLFC				
	65				
Qy	1144 ELEEGFNPCVGEPSLCTMYEGDGETPEPRKRTSIDVCGITYPFKGVLDMQATPAYSHEHKK				
	1203				
Db	66 RQEVSFNFCIDBPSKCYFHDGCVGEFEQKRTSIDCVVITPQGLDPMASNAVSXHO-Q				
	124				
Qy	1204 KCPVSLVTAGEP-HSLICTSYNHPDLPNRPLTGMPEPCVASENETQDDRSBQEGSLKDEE				
	1262				
Db	125 QCPBMTIIGQPAASQVCKTKVIDSEGISQHAMVPCITISVPSQ-----IAQTT				
	173				
Qy	1263 VMLKVCNRRPGEARAIPIFLTTDGLVGEHQDPVTLYLTDVGRSNHSLGTIGLSCQNP				
	1322				
Db	174 FWMIAVSSQPMVAANVIVHLVTDGTGYGDKQKEFTISVQLDITKQSHDLGIHVLSCRRNP				
	233				


```

Db      2443  SPTI-ICQADSTWSPLECEVPECEPQEBELNGIHHVQGLAYLSTLTLYTCKPGRELVG- 2500
Qy      1353  SAVVL--RTSSRIG--LSASNCISBEGQNHQ-----GQ-----1383
Db      2501  NATTLCEGNGMGLGKPKCKPIECPEPEKILNGQFSSVFGYQYITTYFCDRGRLEBPK 2560
Qy      1384  --SCIHPRCGKQDSCPILLDHADVNTCSIGP--GLMKCA-----ITCGRPAI 1429
Db      2561  SLTLE-TEWDMDP--PSCDAHCSDPQPIENGVEGADRYGAMITTYSCPFQV 2614
Qy      1430  QASSQGYIRPMQKELLTCCSSGHW-DQNVSCLPVDCGVD-----1468
Db      2615  LGHAMQ-----TCESGWSSSPTCVPIIDCGAPRIHDQDCTKVRDGGCHPDQ 2663
Qy      1469  -----PSLVYANFSCEBGTFL--KRCISISCVPAKLOGLSPILT 1507
Db      2664  DDMMEVPLAHPHLEATAKALENTKESPAASHFLGTWVSYSCEPGEYLGI-PVLI 2722
Qy      1508  CLEGLMSLPVYC-KLECDAPRIILNANLLPHCLQDNHDVGTICKYCKRGGYVVAESA 1566
Db      2723  QCBGTMMGTAPSCISIECDLPVAPENGFL--HTQT--MGAHQYSCRGHILBSH 2777
Qy      1567  EGVYRNKLLKIQCEGGIWEQGS--CIPVYCEBPVPVFBG-----MYECTN 1610
Db      2778  -----LRL-CLQNKQW-SGTVPRCALISCKNPLMNGSIKGDYSLVGLYECDS 2827
Qy      1611  GFSIDSCVLCNQBREKLPILCTKEGLMTQEPKLCENLOCECPPEBELN-----1661
Db      2828  GYIILNKKRKTQENRD-----WDGHEPNC--IPVDCSPVPVPTGRVYKGEEXT 2874
Qy      1662  --SVEYKCEQGY-----GIGAVCSPL-CVIPPSDVMLENITADTL 1700
Db      2875  FOXKITTSRGGLFLEGAARSLCLTNGSWGATPSCHMVRCPAPQV-----NGVADGL 2929
Qy      1701  E-----HMMEPVKVQS--IVCTGRQWHPDVLVHCIGQCEP 1735
Db      2930  DYGFKEVAFHCLGEGYVLQGAARLTCCQNGTMDAE-----VPCKP 2970

RESULT 6
US-09-911-842A-2
; Sequence 2, Application US/09911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842A
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 3571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-842A-2

Query Match      3.4%; Score 330.5; DB 4; Length 3571;
Best Local Similarity 19.9%; Pred. No. 3.6e-18;
Matches 353; Conservative 207; Mismatches 612; Indels 603; Gaps 106;

Qy      286  AFTVEAWYKPEGQNNPAIAGVFNCSHT--VSD-KGMALGIRSGDKGRDARFFS 341
Db      1450  ALTCTFMWKKSSDDMNYGTPISYAVDNGSDNTLLTLDYNGWLVLYV-NGREK-----1498
Qy      342  LCTRVKATATLILSHSRQPGTWTHTVATYDGRH--MALYVDCQVVASLDSGRLNPF 399
Db      1499  -----ITNCPVNDGRMHIALITWTSANIKWYIDGKISDGGAGLSVGLPIF- 1546
Qy      400  MASCRSLILGSDSEDGHYFR-----GHLGTLVFWSTAL--PQSHFQHSQHSNGEERAT 452

```

```

Db      1547  --GGGALVTLQEBQDKKKEGSPAPSEFVGSISQULMMDYVLSPPQ--QVKSILATSCPEBLS 1601
Qy      453  DLVLTAFEPENVTWVFR-----DEK-----YPRL-----EVLQ-----482
Db      1602  KANVLA-----WDFSLGIVGKVKIDSKSIFCSQCPRLGGSVPHLRTASDELKQSK 1653
Qy      483  -----GF-----BPEP--ELISLPRL-----CGQTV- 503
Db      1654  VNLFCDGFGVLQVGNPVQYCLNQGGWQTPRLPHCERLISGQVPPLENGFHSADDFYAGSTVT 1713
Qy      504  --CNVELISQYNGYWPRLRSGKVIRQVAVNI CDDEGLNPLYSEQIRLOHEALNEASRY 561
Db      1714  YQCN-----NGYULLGDSRM-----FCTDNGSMWNGSPSCLPVDECAVSDCSEH 1758
Qy      562  NISQQLSVHQYHNSTLHRRVLVNCBESKIGN-DHC-DP-BCE--HPLGYDGDQRLQ 615
Db      1759  -----ASCLNVDGS-----YICSVPPYTGDKNCAEPLKCAKPNBENGSHSGELTYTV 1807
Qy      616  G-----RCYSWNRDGLCHYEC-----NNMLANDPDGDCDDPOVADVVRKTCFDPDSPKR 664
Db      1808  GAVTFSCQSGYQLMGVTKITCLESGEMNHL-----PYCKAV--SCGKPAIPEN 1855
Qy      665  AYSVKELKALQINSTHPLNIYFASSVRBDLAGAATWMDKDAVTHLGGIVLSPAYGM 724
Db      1856  G--CIEELATFGSKVTVYRCNKGYTLADKSSCLANSSWSHSP--VCEPVCSS 1907
Qy      725  RGHDTMIHVGAVHLGLYHNFKGVSEBSCNDPCKEYVPSMETDLCADTA-----P 776
Db      1908  PENINN-----GRY-TLSGLTYLSTASYSC-DGYSLQGGSIIECTASGIMWDRAP 1956
Qy      777  TPKSELCREPEPSTDC--GFTFPGARFTNYSYTDNCTDNFTPNQVAMCYLDL 832
Db      1957  ACHLVFGEPRALIDAVITGNFT-----FRNTVYT--CKEGYTLAGDTIECLAD- 2006
Qy      833  VYQQWTSRK--PTPIPPMVTIGQTNKSLITHTMLPISGVVYDRASGSLCGACTEDGT 889
Db      2007  --GKMSRSDQCLAVSCDEPPIVDHASPE--TAH-----RLFGLDAFYCYSDG- 2050
Qy      890  PROVYHTASSRRVCDSSGYWTPREAVGPRD-VDPQCE--PSLOAMSPENVLYHMMNTVPC 946
Db      2051  --YSLADNSQLCLNAGQKVPPEGDMPCIAHFCEKPSVS-----YSI-----2093
Qy      947  PTEGSELLEFQHVQADTLTLMTSEFMSSQVLPTEILLE-----NKESEVHLGPL 999
Db      2094  -----LESVSKAFPAAGS--VVSFKMEGFL-NTSAKIECBRGQGNPSPMSIGCI 2142
Qy      1000  DTFCDIPLTJIKLHVDGKVGKVTTPDERI-----EIDALLTSQHPSLCS 1046
Db      2143  FVRCGEPPSI--MNGYASGSN-YSPGAMAVASCNKGFIYIKGEKSTCEATGQWSSPIPT 2198
Qy      1047  GCRPVRYOVLDRPPFASGLPVVYVTHSHRKFTDVEVTGQWYOVLAVAGSELBASPL 1106
Db      2199  -CHPV-----SCGEPKVENGF--LHTHTGRIPRESVRVQCNPGYVSQSPV 2242
Qy      1107  -----NHIG-APY-----CG-----DGKYSERLGEBCDDDLVSGDCS 1140
Db      2243  FVCGANRHHMSESLMVCVPLDCCGKPRPIQNGFMKGEMFEVGSKYQFCNBEVELVGS-S 2301
Qy      1141  KVCELEBGFNCVGPESLCYMEGDGICEPE-----RKTSLVDCGIYT--PK 1185
Db      2302  WTCQKSGMKNKSNPK-----CMPAKCPPEPPLLENOLVKELETTEGVVTFSGKE 2351
Qy      1186  GYL-----DQMATRAYSHHDKKKCPVSLVTEGPHSLICTSYHNDLPN--HR 1230
Db      2352  GHVILQGSVLKCLPSQW-----NDSFPVCKVLCTPP--LISFVPPISSALHF 2400
Qy      1231  PLTGMPFCVAS--ENETODRSEQPEGSLKEDEVW--LKYCFNRGPARAIFILY 1283
Db      2401  GSTYKSCVGVGFLRGNST-----TLQGDGTWSSPLPEC-----2435
Qy      1284  TDGLVPEHQOP-TVTLVLTVDVRSNHSGLTYGSLSCQHN-PLIINVT--HQNVLPFH 1337

```

```

Db 2436 ----VPECPQPEBEPNGIIDVOGLAY-LSALYTCCKGFELVGNNTTLGEGNHMLGK 2490
Qy 1338 TTSVLNFPSPRVSISAVALTSSRIGLSAPSNCLSEBEGNHOGOS---CIHPCGKOD 1394
Db 2491 PTCALICLKEKELINGKFSYTDLHYGTATYSC--NRGRLGSPSALTLE--TGWD 2545
Qy 1395 -SCPSLLDHDVNVCTSIGP---GLMKCA-----ITCGRFALQASGGYIRPMQ 1441
Db 2546 VDAPS-----CNALHCSPPQIENGFBGADYSYGALIIYSCFPGFVAGHAMQ----- 2594
Qy 1442 KEILLTSSGSHMDQNV-SCLPVDCGVP-----DPSLVNY----- 1474
Db 2595 ----TCESGMSSSIPTCMPIDCGLPPIIDFGDCTKLKDQGFEGEDDMVEVPYUTPH 2649
Qy 1475 ----ANFGSSEBTK-----FL--KRCGISCPRAKLOGLSPMLTLEGLMSLP 1517
Db 2650 PPHYLGAVAKTWEKSPATSSNPLGYTWSYTCNPGVELLD-NPPLTLCQBEDGTWNGS 2708
Qy 1518 EBYC-KLECDAPPIILNANLLPHCLDNHDVGTICKCKEKGYYVSAEAGKVRNKLK 1576
Db 2709 APSCGISIECDLPTAPBNGFLRFET-----SMGSAVOYSCKPGHILVGS- 2755
Qy 1577 IQLEGGIWEQGS---CIIPVCEPPPYFEG-----MYECTNGSLDSQCVLN 1621
Db 2756 L-CLENKMGSGASPRCAISCKKENPYMNGSIKGSNTYLTSLTYECDPGY-----VLN 2808
Qy 1622 CNGREKPLICTEGELMTQEFKLCENLQEGCPPPSEBLN-----SVEYKCEQ 1669
Db 2809 GTEHR-----TCODKXWDEDEPIC--IPVDCSSPPVANGQVDEXTFOKELEYCNE 2861
Qy 1670 GY-----GIGAVCSPL-CVIPSDDPMLPENITADTLBHMMEPVK--- 1708
Db 2862 GFLLGARSRYCLANGMSGATPDCVYRCATPP---QLANGVTBGLDGFMEKVEVPHC 2917
Qy 1709 ----VOSIVCTGRROWHPDVLVHCIOQSCBP 1735
Db 2918 HEGYILHGAPKLTGQSDGNMDAE-----IPLCKP 2946

```

```

RESULT 7
US-09-911-842A-5
; Sequence 5, Application US/09911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; FILE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911,842A
; CURRENT FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 5
; LENGTH: 2489
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-842A-5

```

```

Query Match 3.0%; Score 292.5; DB 4; Length 2489;
Best Local Similarity 19.1%; Pred. No. 4e-15;
Matches 399; Conservative 211; Mismatches 691; Indels 745; Gaps 109;

```

```

Qy 76 GNYLRPYVGEQIHTHTGRSKPDTEGNAVSLVPPDLTENPAGLNGAVEBPAAVPWGDSP 135
Db 434 GKPLEVPPFG-KAVNYPCDHPD-RGTSFDLI-----GSTIR-CTSDPGANGWSSPA 484
Qy 136 GQEBLLD---DDAYLGNQSKESLGRAGIQKGSAMAATTITA---IFTTLN-EKPER 187
Db 485 PRGGLIGHCAQPHFL-----FAKLTQTNASDPDPIGSLKKECRPEY 527
Qy 188 ORGMAKSRQRRQVWKRAEDGQDGSISHPQWPGHSLKHRYKKSPPRESN----- 240

```

```

Db 528 YGRPFSITCLDNLVWSS-----PKDVCKRKSCKTPPDVNGVNHVIT 569
Qy 241 --QNGEGSREATFNSQVC--LPILYSGRRRLRLPREVLAEIREATVEANWKP 296
Db 570 DIQVSRINY-SCITGRLIGHSSAECILSNAAMWSTKPIICORIPGL----- 618
Qy 297 GQGNPAILIGVFNCSHTVSDKMGALGIRSGKDKGRDAFFPSLCTDRYKKAATILSH 356
Db 619 ----PPTIANGDFISTRENPHYSVYTYRCNPSGGRKV---BEL---VGEPSIYCTS 667
Qy 357 SRYPGTWTHVA-----ATYDGRMALVYDGTQVASSLDQ-----SGP-- 394
Db 668 NDDQVGIWSGAPQCIIPNKCTPRNVENGILVSDNRSLFSLNVEVFRCPQFPWKGR 727
Qy 395 ----LN--SPFMAKCSL-----LLGD-----SSEGGHFRGLG 424
Db 728 VKCOALNKEBELPSCGRVQCPDPDVLHAETQRDKNFSRGOBVFVSCBGYDLRGAAS 787
Qy 425 TLVF-----WSTALYQSHFQHSOHSGBEATDVLTAAPFVNTW---VPFDEKXPR 477
Db 788 MRCTPQGDWSPAP--TCEVKSDDFMGQLNGRVLPVNLQAGAKVDFVCDDEGQ 841
Qy 478 LE-----VLOGFE-----PEPEIL-----SPLOPPLCGQTV---CD 505
Db 842 LKSSASVYCLAGMESLWNSVPVCEQIFCSPSPVINGRHTGRKPLFVFPFGKTVNTCD 901
Qy 506 ----NVELIS-----QYNGWPLRGEKVIRYOVNICTD--DEGLNIVSEBQ 546
Db 902 PHPDRTGSPFLIGESTRICTSDPQNGW---SSPAPRCGLIGHCOAPDHPFLAKLTQ 958
Qy 547 ----IRLOHAEALNEAFSR-----YNISQQL-----SVHQV 572
Db 959 NASDPFGTSLKTCREPEYIGRPSITCLDLVWSSPDCKKRSCKTPRPPVNGMNHV 1018
Qy 573 HNSTLHRVVLVNCESPKIGNDCPECEHPLTGYDGDRCCLQGRCYSMNRDGLC-HVE 631
Db 1019 TDIQVGSRI-----NYSK--TTGHRILGHSSAECILSNAAMWSTKPIICORIP 1065
Qy 632 CNMMLNDPDDGCCDDPOVADVKTCEPDSPKRAYSVKELKALQLNSTHFLNITYASS 691
Db 1066 CG-----LPPTIA-----NGDFIST 1080
Qy 692 VREDLAGAATPMDKXAVTHLIGIVLSPAYGMPGHTDTMHEVGHVGLY-----H 743
Db 1081 NREVF-----HYGSVY---TYRNGSGGRKVFELVGEPSIYCTSNDDVG 1123
Qy 744 VFKVSERESCNPKCKETVPSMETGDLCAADTAFT-----PKSELCR 784
Db 1124 IMGGRAPQ--CIIPNKCTPRNVENGILVSDNRSLFSLNVEVFRCPQFPWKGRYKQ 1181
Qy 785 --EPEFTSDTCGTRPPGAPFTNWSYTDNCTDNFTPNQVAMHCYLDLVYQOWTESR 841
Db 1182 ALNKMEBELPSCGRVQCP--PDVLHAERTQRD-KDNFSPOGEVYVSC----- 1226
Qy 842 KPTPIPIPPNVITQGTNKSILTHMLPRLSSGVYD-RASGSLCAGCTEGTGRQVYHTASSR 900
Db 1227 EPG-----YDLRGAAM--RCTPQGDWSPAPATCEVYK 1256
Qy 901 RVCDSSGYTPPEAVGPPD-----VDQCEPSLQAWSPVHLUYNMNTVPCPTGEGSL 954
Db 1257 SCDDPFGQLNGRVLPFVNIQLAKVDFVDEBQ-----LKSSA- 1297
Qy 955 LLFQHPVQADTLTLWTSFFWESSQVLFTEILLENKSVHLG-PLDTF-----CD 1004
Db 1298 ---SYCLAMESLWNSVPV-CEQIFCSPRPVLPNOR--HTGKFLFVFPFGKAVNTCD 1351
Qy 1005 IPLTLKHVDKXGVGVVYTFDERIEIDALLLSQPH-----SPL-----CSCGR 1050
Db 1352 ----PHPDRTS-----FD-LIGESTRICTSDPQNGWSSPAPRCGLIGHCOAPDH 1398
Qy 1051 VRQVLRDPPFASGLPVVYVTHSHRKFTDVEVTGQWQYVLAAGS-----ELGE 1101
Db 1399 FLPAKLTQTNADPFI-----GTSIKYECRPEYVYGRPFSITCLDNLVW 1442

```

```

Qy 1102 ASP-----PLNHIHAPY-CGDGKYSERLGEEDDGLVSGDGCKVCELEBGF 1149
Dy 1443 SSPDVCCKRSCKTRPPDPVNGMVAITDIOVGRINISCTTGHLILGHSSAE----- 1494
Qy 1150 NCVEPSELCTYMEBGDICEPERKTSIVDCG-----IYPKGYLDQMATRAYSSH 1199
Dy 1495 -CILSGTAMHSTPRICQR-----IPCGLPPTIANGDFISTNREHFHSGSVVYTKCN 1546
Qy 1200 EDKCKCPVSLVTEGPHSLICTSYHPD-----LPMH-RPLTWMFPCVASSEMETQ 1246
Dy 1547 LGSGRKRVFELVGP-STYCTSNDDQVIGSGPARQCTIPNKCCTP-----PWNENGLIIVS 1600
Qy 1247 DDRSEOGESLKKEDVWLKVCNRPGEARAIFILTDGLVPGSHOQPTVLYLTVDVG 1306
Dy 1601 DNRS--LFSLNEVEFRCCQGFVWKGR--VKQALNKMPELPGSCSRV----- 1646
Qy 1307 SNHSLGYGLSCQHNPLIINVTH--HONVLPHHTSVLNFSSPRVGISAVALRTSSRI 1363
Dy 1647 -----CQPPPELHGEHTPSHQD-----NFSR----- 1668
Qy 1364 GLSAPNSCISREBQNGOCSCIRPCSKO-----DSCPSLL-LDHADVNC 1409
Dy 1669 GQEVFYSC--EPGYDLRGAASLH--CTPQGDMSPEARCAVKSCDPFLGQLPHGRVLP 1723
Qy 1410 TSIGPLMKCAITCQGFALQASSGOYIRPWKEILLTSSGHWDOVNS-CLPYDCGVPD 1468
Dy 1724 LNLQLG-AKYSFVCDDEGRLLKSSVSH-----CVLWMSLWNNNSVPVEHIFCPNP- 1774
Qy 1469 PSLVNVPNFCSEGT-KFLKRCSTSCVP-----PAKLGSLPMLTCLD-----GLMSLP 1517
Dy 1775 PALNGHHTGTPSGDIPYKEISYTCDBPHDRGMTFNLIGBST-IRCTSDPHGNGVWSSP 1833
Qy 1518 EYVCKL-----ECAPPIIANLILPHCLD-NHDVCTCKECKCPYVVAEABEGNR 1571
Dy 1834 APRCELSVRACHCTPQFPFASPTTP--INDPEPVGTSINVCRRPGYF----- 1881
Qy 1572 NKLKIOCLEGGIME--QGSCTPVUCEPFPVFEFGM-----YECTNGSL- 1614
Dy 1882 GKMSISICLENLVMSVBDNRKRSCEPPEPFGMHINTDQPGTVMVNSCHBGRFLI 1941
Qy 1615 ---DSQVLNCOBREKLPILCTYEGMTQFKLCENIQGECPPPSSELSN----- 1662
Dy 1942 GSPFTTCLSGNNV-----TWKCAPICEIT--SCBPPPTISNDGFYSNNRTS 1987
Qy 1663 -----VEYKCEQYG-----IGAVCSP-----LVYIP-S 1666
Dy 1988 FHNQTVVYQCHTGPDEQLFELVGEBSICTSKDOVGWSSPPRCISTNKCTAEBVE 2047
Qy 1687 DPVVLPEKIT---ADTLEHMEP---VKVQSICTGRQMHDPVVLHGIQSCEP 1735
Dy 2048 NAIIVPNRSPFSLTEIVRFRQGFVWVGSHTVQCCQNGRM--GPKLPHCSRVCQ 2102

RESULT 8
5256642-10
; Patent No. 5256642
; APPLICANT: PEARON, DOUGLAS T.; KLOCKSTEIN, LLOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F., III; STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C., JR.
; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
; RECEPTOR 1 (CR1) AND A THROMBOCYTIC AGENT, AND THE METHODS OF
; USE THEREOF
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,128
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532

```

```

; FILING DATE: 01-APR-1988
; SEQ ID NO:10:
; LENGTH: 1847
5256642-10

Query Match      2.9%; Score 287.5; DB 6; Length 1847;
Best Local Similarity 19.1%; Pred. No. 6.6e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

Qy 454 LVLTASPEPVNT-EMVFP-----RDE-----KYPRLEVLQGEPEPELISPLQPPV-- 498
Dy 39 LALPVANGQCNAREMLFPAPRTNLTBEPFPIGTYLNEYCRPGSGRPPSILCKNSVMT 98
Qy 499 -----CQQTVCN-----VELISQYNGVPLRGEKYI 525
Dy 99 GANDRCGRKSCRNPPDPVNGVHVYIKIGFGSQIKYCTKGRLIGSSATCISGTVI 158
Qy 526 RYOVNVCID--DEGLNIVSEBQIRLOHEALNEAF--SKYINSMQSLVHQNSTLHR 580
Dy 159 WNETPICDRIPCGLPPTIT-----NGDFISTNRENFY-----GS 194
Qy 581 VLVNCSRSKIGND-----HCDPECEHPLTGYDGG--DCRLQRCYSWNRBDGL 627
Dy 195 VVTRCNPSGSGRKRVFELVGEPSIYCTSNDDQ--VGWSPARQCTIPNKCCTPENVANGI 252
Qy 628 CHVECNMM--LNPFDGDC-----C-----DPOVADVKTGCPDPSPRAY 666
Dy 253 LVSDNBSLFLSLENEVEFRCCQPFVFMKGRPRVVKCOALNKMPELPGSCSRVCO 311
Qy 667 MSVKELEKALQIINSTH--LNTYFASVREDLAAGATV-----PMDKNAV----- 710
Dy 312 -----ERTORDNDNSPQGEVFFYSCEPGYDLRGAASMCCTPGQDMSPAAPTEVKS 364
Qy 711 -----HLGIVLSPAYVGMPTDTMINEVGHVLG--LVHVPFG-----VSERE 752
Dy 365 DFMGQLNGVLPFPVNIQLAKVDVFCDBGFLKSSASICVLAGMSLWNSVPCBQI 424
Qy 753 SCNDPCKEYPS-METG-----DLCAD----- 773
Dy 425 FC--PSPFVLPNGHGTCKPLEVFPFGKAVNYTCDPHDPRTGTFDIEGSTRCTSDPGN 482
Qy 774 ---TAPPKBEL--CREP-----PTSDTCGTRFP--GAFTYMS 808
Dy 483 GWSSPAPRGGIIGHCOAPHFLEPAKLQTNASDPFISGLKCEKCEYVGRFSS----- 538
Qy 809 YTDNCTDNF--TPNOVAMHCLDLVQOMTESRRTPLPIRPVY----- 852
Dy 539 ---ITCLDNLVWSSPKDVC-----RKSKTPDPVNGMVAITDIOVGRIN 583
Qy 853 -----IGQTKSLTI-----HW--LRPI-----SGVVYDRASGLCGACTEDGTFR 891
Dy 584 YSCCTGHRLLGHSAEELISGNAMHSTKRPICQRIQGLPPTIANGDFI-----STNR 637
Qy 892 QYVHTAS--SRVCDSSGYWTPREAVGPEDV-----DQCEPSQLQMS--PEVNLVMMN 942
Dy 638 ENFYGSVVTVYRCNPGSGGRKRVFELVGEPSIYCTSNDDQ-----VGWSPARQCTIPN 692
Qy 943 TVPCPTGSGLELLFQRPVQADTLTLMVTSFPMSSQVLTFTBILF--NKSIVHLG 999
Dy 693 CTPEPNE-----NGLIVSDNBSLSLNEVVFRCQPGVVMGGR 731
Qy 1000 DTFCDIPLTKLHVQKVGKVVYTPDERIEIDALLTTSOPHSPBLSG--CRPVYQVLRD 1058
Dy 732 RVKQ-----ALNKMPELPGSCSRVCO----- 754
Qy 1059 PPFASGLPVVYVTHSHRKFTDVE--VTPQOMQYOVUAAAGBL-GEAS--PLNHIHGA 1112
Dy 755 -----PDLVLAERTQDKDNFSPQGEVFFYS--CEPGYDLRGAASMCRTPGQDMSPA 805
Qy 1113 PYCG-----DGK-----VSERLGE-----CDGDLVSGDGS----- 1140
Dy 806 PTEVKSCTDFMGQLNGRVLPVNIQLAKVDVFCDBGFLKSSASICYVLAMESLWN 865

```



```

QY 1141 ---KVCE-----LE-----EGFNCVGPSP-L-C 1158
D 866 SSVVCEIOIFCPSPVPVLPNGHNTGKPLEVFPFGKAVNTCDPHDRKGSFPLIGESTIRLC 925
QY 1159 YM-YEGDGI-----CE-----PEERKTSIVDCGIYT-----PKGY-- 1187
D 926 TSDPOGNGVWSPAPRCGLIGHCOAPDHFPAKLKTQGNADPFIQTSLKKECCPEYVGR 985
QY 1188 -----LDONATRAYSHED---KKKC--PVSITYGEPHSLI-----CTSHPD 1225
D 986 PFSITCLD---NLVWSSPKVDCKRKSCTPPDPVNGMWHVITDIQVGRINYSCTTGH-R 1041
QY 1226 LPNHR-----PLTGWPPC-----VASENETODDRSPEGSLKXEDV 1263
D 1042 LIGHSABEILISGTAHMTSTPPIQCRIPGCLPPTIANGDPISTNREHFGSV----- 1095
QY 1264 WLKVCNRPGEARAF-----IFLTDDG-----LVPGHQOPTYT---LYL 1301
D 1096 -VTVRCULGSRGRVFLVGEPSIYCTSNDDQVIGWSGAPQCIIIPNKCTPPVENGILV 1154
QY 1302 TDVRGSHSL-----GTYGLSGQ-----HNPLIINTVTHHQNVLFF 1336
D 1155 SD-----NRSLEFLNEVDFRCQPFVWKGPFRVRCQALNKWPELPSCSRVCOPEPILH 1210
QY 1337 --HTSVLANPSSPRVGINAVALTSSRIGLSAPSNCSDEGQNHQOSCIHRPCGQ- 1393
D 1211 GEHPSHODNFS-----GQEVFYS- -BPGYDLGAAALH--CTPQG 1249
QY 1394 -----DSCPSLL--LDHADVNCSTISGILMKCAITTCORFALQASGQYIRPM 1440
D 1250 DMSPEARCAVKSCHDDFLGQPHGRVLEPLNLQIG-AKVSFVCEBGRKKSYSVSH----- 1304
QY 1441 QKEILLTCSSGHWONVS-CLPVDGVPDPSELVAVNFSCSEG-TKELKRCISICVP-- 1495
D 1305 ---CVLWMSRLMNNSVFVCEHIFCPNP-PAILNGRHGTGPSGDIPIYKEISYTCDPHPD 1360
QY 1496 ---PAKQIGSPMLTCLD---GLMSLPEVYCKL-----ECDAPIILMANLLPHCLQ 1543
D 1361 RGMFTNLIGEST-TRCTSDPHGNGVWSPAPRCBLSVRAGHCKTPEOPFPFSPTIP--IN 1417
QY 1544 D-NHDVGTICKECKPGYVAVESAEGKVRNKLKIQCLEGIME--QSCCIPVVCPPPP 1600
D 1418 DFEPRVTSILNBERPGTF-----GCMPSISCBENLVMSVEDNCRKSCGPRPE 1467
QY 1601 VFBSM-----YECTNGFSL---DSQCVLNCQBERKLPILCTKGLMTQE 1642
D 1468 PFNGMWHINTDTQGSTVYVSCNEGFRLLIGSPSTCLVSGNNV-----TWDKK 1515
QY 1643 FKUCENIOGECPPPPSELNS-----VEYKCEQGYG----- 1672
D 1516 APICEII--SCEPPTISNGDFYSNNRTSFNGTUVVYQCHTGPDGQLFELVGRSIIYC 1573
QY 1673 -----IGAVCSP-----LCVIIP-SDPVMLEPENT---ADTLEHMMER---YKV 1709
D 1574 TSKDDQVGVWSSPPRCISTKCTAFAVEYNAIRVGNRSFSLTEIIRFCQGFVWGS 1633
QY 1710 QSIIVCTGRQMPDPVLVHCIOSEP 1735
D 1634 HTVQCQTNGRW--GPKLPHGSRVCOF 1657

```

```

; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588, 128
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 412, 745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332, 865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176, 532
; FILING DATE: 01-APR-1988
; SEQ ID NO: 10
; LENGTH: 2006
5472939-10
Query Match 2.9%; Score 287.5; DB 6; Length 1847;
Best Local Similarity 19.1%; Pred. No. 6.6e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

QY 454 LVLTASPEPVNT--EMVFP-----RDE-----KYPLEVLQGEPEPEILSPLOPL-- 498
D 39 LALPVMAGCCNAPWMLFPAAPTLNLTDEFFPIGYLNYECPRGYSGRPFSIICLKNSVWT 98
QY 499 -----CGQTVCDN-----VELISQYNGYMPLRGSKYI 525
D 99 GAKDRCKRKSCHNPDVNGMWHVYIKGIQFSQIKYSCTKGYRLIGSSATCIIISGPTVI 158
QY 526 RYQVNVICD--DEGLNIVSEBQIRLOHEALNEAF---SRYNISWQLSHVQVHNSITLHR 580
D 159 WNETPPICDRIPCGLPPTIT-----NGDFISTNENFHY-----GS 194
QY 581 VVLVNGEPRKIGND-----HCDPECHPLTYGDDG---DCRLQRCYSWNRBDGL 627
D 195 VTVRCNPGSGGRKVFELVGEPSIYCTSNDDQ--VGIWSGAPQCIIIPNKCTPPVENGIL 252
QY 628 CHVECNMM--LNDPDDDC-----C-----DQVADVKTCEPDSPKRAY 666
D 253 LVSDNRSLFSLNEVBERCQPFVWKGPFRVRCQALNKWPELPSCSRVCOPEPILH 311
QY 667 MSVKELEBALQIQLNSTH--LNTYFASVREDLGAAATW-----PYDKAVT----- 710
D 312 -----ERTQORDNNSPQGEVYFSCPEGYDLGAAASMRCTPGDWSPAAPTEVYKSCD 364
QY 711 -----HLGGIVLSPAYYGMGHTDTMIEVGHVUG---LVYVFGK-----VSERE 752
D 365 DFMGQLNGKVLFPVNIQIQAKYDFVCDGFGQLGSSASIVLGLMSLNNSSVPCEQI 424
QY 753 SCNDPCKETVPS--METS-----DLCAD----- 773
D 425 FC--PSPVLPNGHNTGKPLEVFPFGKAVNYTCODPHDRGTSFPLIGESTIRCTSDPQGN 482
QY 774 ---TAPPKSEL--CREP-----PISDTGCTTRP--GAPFTYMS 808
D 483 GWSSPAPRCGLIGHCOAPDHFPAKLKTQGNADPFIQTSLKKECCPEYVGRPFS----- 538
QY 809 YTDNCTDNF---TRNOVAMHCYLDLVYQOMTESRKTPIPIRPNV----- 852
D 539 ---ITCLDNLVWSSPKVCK-----RKSKCTPPDPVNGMWHVITDIQVGRIN 583
QY 853 -----IGQTNKSLTI-----HM--LRPI-----SGVYUDRASLSGACTEDGTFR 891
D 584 YSCCTGHRILGHSAEILISGNAHMTSTPPIQCRIPGCLPPTIANGDPI-----STNR 637
QY 892 QYVHTAS--SRRVCDSSGYWTPBEAVGPVDV-----DQCEPSLQWS--PEVHLVHNM 942
D 638 ENFHYGSVVTVYRCNPGSGGRKVFELVGEPSIYCTSNDDQ-----VGIWSGAPQCIIIPNK 692
QY 943 TVPCPTGSLLELFGHPVQADTLTAVTSFPMSSQVLPOTEILLE---NKESVHIGPL 999
D 693 CTPEPNT-----NGILVSDNLSLSLNEVFPFCQPFVWGR 731
QY 1000 DTFCDIPULTIKLVHGKVSQVYVTPDERIEIDALLTSSQHPSPKSG--GRPVYQVLRD 1058
D 732 RVKCG-----ALNKWPELPSCSRVCOF----- 754

```

```

QY 1059 PPFASGLPVVTVTHSHRKETDVE-VTPGOMYOYOVLAENAGEL-GRAS-----PPLNHINGA 1112
D 755 -----PPVTLHERTQORDKDNSSPGGEVYFS-CERGYDVLGAASMRCTPQGMWSPA 805
QY 1113 PYCG-----DGK-----VSEKGEF-----CDGDVLSDGDCG----- 1140
D 806 PTCVKSQCDPMGQLNGRVLFPVNLQGAQVDFCDBEQGLKSSASAYCVLAEMESLMN 865
QY 1141 ---KVCE-----LE-----EGFNCVGPBSL-C 1158
D 866 SSVAVCEQIFPCPSPVLPNGRHTGKPLEVFPFGKAVNTCPDPHPRKGSFPLIGESTIRC 925
QY 1159 YM-YEGDGI-----CE-----PEPKTSIVDCGIYT-----PKGY-- 1187
D 926 TSDQGMGWSSPAPRGILGHCAQDHFLEPAKLKTQTNADPFIQTSLKVECPREYGR 985
QY 1188 -----LDQATRAYSSHED---KKKC--PVSLVTGEPHSLI-----CTSYHPD 1225
D 986 PPSITCLD---NLVWSSPKDVCKRKSCKTPDPVNGMVHVTIDIOVGSRLNYSCTTGH-R 1041
QY 1226 LPNHR-----PLTGWPC-----VASENETODDRSQRPGESLKKEDEV 1263
D 1042 LIGSSAECLISGNTAMSTKPPICQRLPCGLPPTIANGDITSTNRENTFYGSV----- 1095
QY 1264 WLKVCFNRPGEARAIF-----IFLTIDG-----LVPEGHQOPTYT--LYL 1301
D 1096 -VTRCNLGSRGKRVFELVGPBSIYCTSDNDQVIGWSGAPAQCIIPNKCTPENVENGILV 1154
QY 1302 TDVAGSNHSL-----GTYGLSQ-----HNPLIINTHHQNVLFH 1336
D 1155 SD-----NRSLSFLNEVVDFRCPGFVWKRPBRVQCQALNKWPELPPSCSRFCQPPPELILH 1210
QY 1337 -HTTSVLNSSPRVIGSAVALRTSRIGLSAPNSCISEDEGNOHOGSCIHPRPCGKO- 1393
D 1211 GEHTPSHODNSP-----GQEVFISC---EPGIDLKRAAAILH--CTPQG 1249
QY 1394 -----DSCPSLIL--LDHADVNVCTSIGPLMKCAITTCRGFALQASQOYIRPM 1440
D 1250 DWSPEARCAVKSDDFLGQLPHGRVLEPLMLQIG-AKVSPVCEBGFLLKSSVSH----- 1304
QY 1441 QKEILLTCCSGHMQONS-CLPVDGQVDPBSLVYANSSCSG--TKFLKCSISGVP-- 1495
D 1305 ---CVLVGMRSLMNNSVFVCEHIFCPNP-PAILNGRHTGTSGDIPYKELISYCDPHPD 1360
QY 1496 ---PAKLGSLPWLTCLED---GLMSLPEVYCKL-----ECDAPPIILNANLLPHCLQ 1543
D 1361 RGMTPNLIGEST-IRCTSDPHGNVWSSPAPRCESLVAGCKTPEQPPFASPITP--IN 1417
QY 1544 D-NHDVGTICKYECKPGYVAESAEGKVRNKLKIQCLEGGIWE--QGSCLPVYCEPPP 1600
D 1418 DFEFPVGTSLNYECRPGYF-----GKWFISICLENLWSSVEDNCRKSCGPPPE 1467
QY 1601 VFEBGM-----YECTNGFSL---DSQCULNCQBERBKPLILCTKSGLTQOE 1642
D 1468 PFNGMVHINTDQFGSTVNVSCNGBFRLIGSPITCLVSGNNV-----TMDKK 1515
QY 1643 FKLGNLQGECPPPSELNS-----VEYKCEQYGV----- 1672
D 1516 APICEIIT--SCEPPPTISNGDFYSNNRKSFPANGIVVITYQCTGPDGDEGLFELVGBRSIYC 1573
QY 1673 ---IGAVCSP-----LCVILP--SDPVMLPENIT--ADTLEHMMPE---YKV 1709
D 1574 TSKDQYGWSSPPRCISTNKCTAPAEVENAIRVGNRNSFSLREIIRFRQGPFWVWGS 1633
QY 1710 QSIIVCTGRQWHPDPVLVHCTIQSCGP 1735
D 1634 HTVQCQTNGRW--GPKLPHCSRVCP 1657

```

RESULT 10
5256642-10
; Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,

```

; MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; ID, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
; RECEPTOR 1 (CR1) AND A THROMBOTIC AGENT, AND THE METHODS OF
; USE THEREOF
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/589,128
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1988
; SEQ ID NO:10:
; LENGTH: 1847
5256642-10

```

Query Match 2.9%; Score 287.5; DB 6; Length 1847;

Best Local Similarity 19.1%; Pred. No. 6,66-15;

Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

```

QY 454 LVLTASEPEVNT-EWVF-----RDE-----KYRLEVLQGEPEPELISPLQPL-- 498
D 39 LALPVAQGNAPAEWMLFPAPPTNLTDDEFEPPIGTLYNVECRPGSGRPFSLICLKNVMT 98
QY 499 -----CGQTYCDN-----VELISQYNGWPLRGKVI 525
D 99 GAKDRCKRCKRPPDPVNGMVHVIKGIQFGSQIKYSCYGRYLIGSSATCIISGTVI 158
QY 526 RYGVNVCID--DEGLNIVSEBOIQLQHEALNEAF--SRYNISWOLSVHQNSTLRHR 580
D 159 WDNETPICDILPCLPPTIT-----NGDFISTNNENFIY-----GS 194
QY 581 VLVNCEPSKIGND-----HCDPECEHPLTGYDG--DCRLQGRCYSMNRDGL 627
D 195 VVTRCNPSGSGRKFELVGPBSIYCTSDNDQ--VGIWSGAPQCIIPNKCTPENVNGI 252
QY 628 CHVEGNM--LNDPDDDC-----C-----PQVADVAKTGEDPSPRAY 666
D 253 LVSDNRSLFSLNEVEVERCPVFVWKRPBRVQCQALNKWPELPPSCSRVCPDPDLHA- 311
QY 667 MSVELKEALQLNSTHP---LNIYFASVREDLAGAATW-----PMDKAVT----- 710
D 312 -----ERTQORDKDNSSPGGEVYFSCEPGDILGAASMTCTPQGMWSPAAPTECVKSCD 364
QY 711 -----HLGIVLSPAYYGMDGHTDTMIEVGHVIG--LYHVEKG-----VSERE 752
D 365 DFMGQLNGRVLFPVNLQGAQVDFVCEGFLKSSASAYCVLAEMESLMNSVFPCEQI 424
QY 753 SCNDPCKEYPS-METG-----DLCAD----- 773
D 425 FC--PSPPVLPNGRHTKPLEVFPFGKAVNYTCDPHDRGTSFPLIGESTIRCTSDPQGN 482
QY 774 ---TAPPKSEL--CREPE-----FTSDTCGTRPP--GAPFTYMS 808
D 483 GWSSPAPRGILGHCAQDHFLEPAKLKTQTNADPFIQISLAKVECPREYGRFS----- 538
QY 809 YTDNCTDNF--TPNOVAMHCYLDLVQOQWESKRPTPIPLPMV----- 852
D 539 ---ITCLDNLVWSSPKOVCK-----RKSCKTPDPVNGMVHVTIDIOVGSRLN 583
QY 853 -----IGQNTKSLITI-----HW--LPLI-----SGVYDASGLGACNEDGFR 891
D 584 YSCTTGHRLLGHSSAECLISGNAAMWSTKPPICQRLPCGLPPTIANGDPTI--STNR 637
QY 892 QYVHTAS--SRVVDSSGYWTPEBAVGPDPV-----DQCEPSLIQAMS--PEVHLIYHNM 942
D 638 ENFHYGSVVTYTRCNPSGSGRKFELVGPBSIYCTSDNDQ-----VGIWSGAPQCIIPNK 692
QY 943 TVPCPTGCSLELLFQHPVQADTLTLVWTSFMESSQVLFDTETILLE--NKESVHLGRL 999

```

```

Db      693 CTBPNNV-----NGILVSDNLSLFSLNVAFRCQPFVMMGPR 731
Qy      1000 DTFCDDILITKLHVQKVGSKVKTFTFDEBJEIDAALLTSPHSLCSG-CRPNRYQVLRD 1058
Db      732 RVKCO-----ALKMKEBELPSCSRVCOF-----754
Qy      1059 PPFASGLPVVYVTHSHRKTDE-VTPGOMYQYUOLAAAGBL-GEAS-----PLNTHIGA 1112
Db      755 -----PPDLHAERTQDKDNFSPGQEVFTS--CEPGYDLKRAAMRCTPQGDWSPAA 805
Qy      1113 PYCG-----DGK--VSERLGEE--CDGDVLVSGDGS-----1140
Db      806 PTCBEVASCDDPMQGLNGRVLFPNLDLQAKVDFCDEBQOLKSSASVCLAGMESLMN 865
Qy      1141 --KVCE-----LE-----EGFNCVGEPSL-C 1158
Db      866 SSVPVCEQIFCPBPVIPNGRHGTGKPLEVFPFGKAVNYTCDPHDRGTSFDLIGESTIRC 925
Qy      1159 YM-YEGDGI-----CE-----PERKTSIVDCIYT-----PKGY-- 1187
Db      926 TSPDQNGVWSSPAPRCGLGHQCAPDHPFLPAKLKTYTNASDPPIGSLKYECRPEYGR 985
Qy      1188 -----LDQWATRAYSSHED--KKKC--PVSIVTGEPSHLI-----CTSYHPD 1225
Db      986 PFSITICD--NLVWSSPKDYCKRKSCKTPPDVNGMNVHTIDIQVSGRINYSCTTGH-R 1041
Qy      1226 LPNHR-----PLTGMFPC-----VASENETODDREBOPEGLKXEDV 1263
Db      1042 LIGHSASCLISGNTAMSTKPIQRIPLCGLPPTIANGPDISRNENFHYGSV-----1095
Qy      1264 WLKCFRPRGEARIF-----IFLTDDG-----LVPGHQOPIYT--LYL 1301
Db      1096 -VYTRCMJGSRGRKVFELVGPBSIYCTSNDDQVGIWSPAPQCIIPKCTPPNVENGILV 1154
Qy      1302 TDVAGSNHSL-----GTVGLSCQ-----HNPLINVTHTHQVLFH 1336
Db      1155 SD-----NRSFLSLNEVVDFFRCQPFVMMGPRRVKCOLANKKEBELPSCSRVCOFPPBELH 1210
Qy      1337 --HTTSLVILNFSFPRVGISAVALTSSRIGLSAPSNCISSEDEGNOHOGSCIHPRCKGO- 1393
Db      1211 GEHTPSHQDNFSP-----GQEVFTYS--EPGYDLGAGASLH--CTPQG 1249
Qy      1394 -----DSCPSLL--LDHADVNCTSIGGLMKCAITTCORFALQASQOYIRPM 1440
Db      1250 DMSPEARCAVKSCDDELQGLPHGRVLFPLNLQLG-AKVSFVCEGFRLLKSSVSH-----1304
Qy      1441 QKELILTCSSGHMDQNTS-CLPVDGVPDPBSLVVYANFSCSEG-TKFLKCSISCVF---1495
Db      1305 --CVLVGMRSLMWNVSVPVCEHIFCPNP-PAIIMGHGTTPSGDIPIYKKEISYTCDDPHD 1360
Qy      1496 ---PAKQLGSLPWLCTLED---GLMSLPEVYCKL-----ECDAPPIILNANLLPHCLQ 1543
Db      1361 RGMTHPLIGEST-IRCTSDPHNGNVWSSPARCCLSTRAGHCKTPBQPPASPIITP--IN 1417
Qy      1544 D-NHDVGTICKYECRPGYVAESAEGKVRNKLKIQCLEGGIWE--QSSCIPIVVCPEPPP 1600
Db      1418 DFEFPVSTINYECPRGYF-----GKMFSISCIENLWMSVSDNCRKSCGPPE 1467
Qy      1601 VFBGM-----YECTNGPSL--DSQCVLNCQBERKLPILCTKSGMLTQE 1642
Db      1468 PFNGMVAHINTDQFSTVNVSCNGBFRLIGSPSTTCLVSGNNV-----TWDDK 1515
Qy      1643 PKLCEINTQSGCPRPSELNS-----VEYKCEQGYG-----1672
Db      1516 APICEIIL--SCFPPTISNGGFYSNNRTSFHNGVTVVYQCHTGPDDGQLFELVGERSTYC 1573
Qy      1673 ---IGAVCSP-----LCVIPP-SDPVLMPENIT--ADTLEHMMNP---VKV 1709
Db      1574 TSKDQGVWSSPFPICSTIKTAPAEVENAIRVGNRSFSLTEIRFRQCPGFVWYGS 1633
Qy      1710 QSIVCTGRQMHPRPVLVHCIOGCEP 1735

```

```

Db      1634 HTVQCQTNGRW--GPKLPHCSRVCOF 1657
RESULT 11
5472939-10
;PATENT NO. 5472939
;APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; MONG,
;WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
;H.; MAKRIDES, SAVVAS; MARSH, HENRY C., JR.
;TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
;MEDICATED DISORDERS
;NUMBER OF SEQUENCES: 30
;CURRENT APPLICATION DATA:
;APPLICATION NUMBER: US/08/138, 825
;FILING DATE: 19-OCT-1993
;PRIOR APPLICATION DATA:
;APPLICATION NUMBER: 588, 128
;FILING DATE: 24-SEP-1990
;APPLICATION NUMBER: 412, 745
;FILING DATE: 26-SEP-1989
;APPLICATION NUMBER: 332, 865
;FILING DATE: 03-APR-1989
;APPLICATION NUMBER: 176, 532
;FILING DATE: 01-APR-1988
;SEQ ID NO:10:
;LENGTH: 2006
5472939-10
Query Match 2.9%; Score 287.5; DB 6; Length 1847;
Best Local Similarity 19.1%; Pred. No. 6.6e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

Qy      454 LVLTASFEVNT-EWVFP-----RDE-----KYPLEVLQGEPEBELISPLQPPV-- 498
Db      39 LALPVAQGCNAEMLEFARPTMLTDEFEPIGTLYLVNCEGRPGYSFICKNCSWYT 98
Qy      499 -----CGQVYCDN-----VELISQVNGWPLRGKVI 525
Db      99 GANDCRKRSKCRNPDPVNGMNVHYKIQSGOIKYISCTGYRLIGSSSATCIIISGDVI 158
Qy      526 RYGVVNICD--DEGLNFIVEEQIRLQHEALNEAF--SRYNISWQSLVHQNHNSTLHR 580
Db      159 WDNETPICDRIPGLPPTIT-----NGDFISTNENPHY-----GS 194
Qy      581 VLVNCEPSKIGND-----HCDPECEHPLTGYDG--DCRLQGRCYSNRRDGL 627
Db      195 VVTRKCNPGSGGRVFEVFBGPEISYCTSNDDQ--VGIWSGAPQCIIPKCTPPNVENG 252
Qy      628 CHEECNNM--LNDPDDDC-----C-----DPQVADVKTCTDPDPSPRAY 666
Db      253 LVSDNRSLFSLNEVEFRCPQPFVMMGPRRVKCOLANKKEBELPSCSRVCOFPPDVLAH 311
Qy      667 MSVXELKEALQLNSTHF--LNIYFASVREDLAGAATW-----PMDKDAVT-----710
Db      312 -----ERTQDKDNFSPGQEVFTS--CEPGYDLGAGASLH--CTPQG 1249
Qy      711 ---HLGGIVLSPAYYGMGHTDTMIVGHVGLG--LYHVFKG-----VSERE 752
Db      365 DFMQQLNGRVLFPVNLQQLAKVDFVCEGQOLKSSASVCLAGMESLMNSVAVCEQI 424
Qy      753 SCNDPCKEYTPS-METG-----DLCAD-----773
Db      425 FC--PSPBPVIPNGRHGTGKPLEVFPFGKAVNYTCDPHDRGTSFDLIGESTIRCTSDPGN 482
Qy      774 ---TAPPKSEL--CREPE-----PSTDCGTPRP--GAPFTVMS 808
Db      483 GWSSPAPRCGLGHQCAPDHPFLPAKLKTYTNASDPPIGSLKYECRPEYGRFS-----538
Qy      809 YTDNCTDNF--TPNQVARMHCVLVLVQOWTESRKPPIPIPPV-----852
Db      539 ---ITCLDNLVWSSPKDYCK-----RKSCKTPPDVNGMNVHTIDIQVGSRI 583
Qy      853 -----IGQNKSLIT-----HW--LPPI-----SGVVYDRASSSLGACTEDGTFR 891

```

```

Db 584 YSCTTHRLGHSSAECLISGNAHMTKPRICQRIQGLPPTIANQDFT-----STNR 637
Qy 892 QYVHTAS--SRKVDSSGYTTPBEAVGPBV-----DQCEBPLQAMS-PEVHLVHMM 942
Db 638 ENFHYGVVYTRKCPKGGGRKVFELVGPISYCTSNDDQ-----VGIWSGAPQCIIPNK 692
Qy 943 TVPCPTGSGLELLEFQHPVQADTLTLWVTSFPMESSQVLPDTEILLE--NKEGVHIGPL 999
Db 693 CTPNVE-----NGILVSDNLSLFLSNEVVERCQPGFVMMGPR 731
Qy 1000 DTFCDILPLTKLHVDGKVGKVTYFDERLEIDAALLTQSPHPLCSG-CRPVRYQVLRD 1058
Db 732 RVKQC-----ALNKMPELPSCSRVCQ-----754
Qy 1059 PPRPAGLPVYVTHSHRKTVE-VTPQMYQVLAEGSL-GEAS-----PRLNHITGA 1112
Db 755 -----PPVLAHERTORQDKDNPSPQGEVFTS--CEPGYDLRGAASMRCTPGDMSPA 805
Qy 1113 PYCG-----DGK-----VSERLGEE--CDPDGLVSGDGS-----1140
Db 806 PTCVKSQCDPMGOLLNKRVLFPVNLQIGAKVDYCEBGLKSSASYCVLAGMESLMM 865
Qy 1141 ---KVCE-----LE-----EGFNCVGEPSL-C 1158
Db 866 SSVAVCEQIFCPSRPVIPNGRHTGKPLEVPPFGKAVNYTCDPHDRGTSFDLIGESTIRC 925
Qy 1159 YM-YESGCI-----CE-----PREKTSYDCGIY-----PKGY-- 1187
Db 926 TSDQGGWSSPAPRGILGHCOAHPFLPAKTKTQTNADPFIQSLKYCBEVYGR 985
Qy 1188 -----LDQWATRAYSHED--KKKC--PVSALTGEHSLI-----CTSYHPD 1225
Db 986 PFSITCLD--NLWSSPKVDCKRKSCTPRDPVNGMHVITTDQVSGRIYSCITIGH-R 1041
Qy 1226 LPNHR-----PLTGMFPC-----VASENETODRSEBPSLKKEDV 1263
Db 1042 LIGHSABCLISGNTAHMSTKPRICQRIQGLPPTIANQDFTSNREMFHGSV-----1095
Qy 1264 WLKCFNRPGEARLIF-----IFLTIDG-----LVPGHQOPTYT--LYL 1301
Db 1096 -VYTRCNLGSRRKRVFELVGPISYCTSNDDQVGIWSGAPQCIIPNKCTPPNVENGILV 1154
Qy 1302 TDVAGSNHSL-----GTVGLSCQ-----HNPLINVTTHQNVLFH 1336
Db 1155 SD-----NRSLFSLNEVVDRCQPGFWKGPFRVVCQALNKMBELPSCSRVCOPEPILH 1210
Qy 1337 --HTTSVLNLSSPRVGISAVALTSTRIGLSAPSNCISEDEGQNHQSGCIHRPCGQ- 1393
Db 1211 GEHTPSHQDNFS-----GQEVFYSC--EPGYDLRGAASLH--CTPQG 1249
Qy 1394 -----DSCPSSL--LDHADVYNCISIGBLMKCAITCQGRFPLQASSQOYIRPM 1440
Db 1250 DWSDEAPRCAVKSDDFLGQLPHGRVLEPLMLQIG-AKVSVFCDEGFLKSSVSH-----1394
Qy 1441 QKEILLTCSGHWQDONS-CLPVDCGVDPPLVNVYANVSCSEG-TKFLKRSISCV- 1495
Db 1305 ---CVLVGMRSLMNNSPVCEHIFCPND-PAILNGRHTGTSGDIPIYKEISYICDHPD 1360
Qy 1496 ---PAKLGSLPWLCTED---GLWSLPEVYCKL-----ECDAPPIILNALLPHCQ 1543
Db 1361 RGMFNLIGEST-IRCTSDPHNGVWSSPAPRCELSVRAHCKTPEQPPFASPITP--IN 1417
Qy 1544 D-NDHVGTCIKYECKPGYVVAESABGKVRKULKIKIQLGSGIWE--QSCCIPVVCPEPP 1600
Db 1418 DFEPPVGTSLNYECPGYF-----GRMFSISCIENLWSSVEDNCRKRSCKGPPPE 1467
Qy 1601 VEEEM-----VECTNGFSL--DSQCVLNCQREKLPILCTKSGLWTOB 1642
Db 1468 PFNGVHINTTGTGSGTYNISCNEGFRLIGSPSTICLVSGNNV-----TMDKK 1515
Qy 1643 FKLCENLQGECPPEPSBLNS-----VEYKEQGYG-----1672

```

```

Db 1516 APICEII--SCBEPPTISNGDFYSNNRTSPFNHGVTVYQCHTGPBGQLFELVGERISYC 1573
Qy 1673 -----IGAVCSP-----LCVIP-SDPVMLPENIT-----ADTLEHMMPE--VKV 1709
Db 1574 TSKDDQVWSSPPEPRCISTNKCTAPBEVENAIRVGNRSFSLTEIRFCQPGFVWGS 1633
Qy 1710 QSIYCTGRQWHPDPVLVHCIOGCEP 1735
Db 1634 HTVQCCQTNGRW--CPKLPHCSCRVCQ 1657

RESULT 12
5256642-2
Patent No. 5256642
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; MONG,
MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CRI) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO:2
LENGTH: 2039
5256642-2

Query Match 2.9%; Score 287.5; DB 6; Length 2039;
Best Local Similarity 19.1%; Pred. No. 7,7e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

Qy 454 LVLTASFEPIVNT-EWVPF-----RDE-----KYRPLEVLQGEPEPEPLISPLQPL- 498
Db 34 LALPVVAGQCNAPLWLFAPFAPNLTLDEFPPIGTYLNEBCRPGSGSPSTICLANSVWT 93
Qy 499 -----CGQTYCDN-----VBLISQNGYWPJRGEKVI 525
Db 94 GANDRCRKSKRNPDPDVNGMWHVYIKIQSGQIKYCTGKRYLIGSSATCISGTVI 153
Qy 526 RYQVNICD--DEGLNIVSEBQIRLOHEALNEAF--SRYNISWQLSVHQNSTLHR 580
Db 154 WDNETPICDRIQGLPPTIT-----NGDFISTNRENFHY-----GS 189
Qy 581 VVLVNERPSKIGND-----HCDPECHPLTGYDG--DCRLQGRCYMNRBDGL 627
Db 190 VVYTRCNPSGGGRKRVFELVGPISYCTSNDDQ--VGIWSGAPQCIIPNKCTPPNVANGI 247
Qy 628 CHVECNMM--LNPFDDEDQ-----C-----DPOVADVAKTGFDPDPSPRAY 666
Db 248 LVSDNRLSFLSNEVVERCQPVFMKGPFRVVCQALNKMBELPSCSRVCOPEPDLHA- 306
Qy 667 MSYKELKALQLNSTHE--LNIYFASVREDLAAGATW-----PMDKDAVT-----710
Db 307 -----ERTQDKDNPSPQGEVFTSCEPGYDLRGAASMRCTPGDWSPAPFCEVXSCD 359
Qy 711 -----HLGIVLSAYVGMGHDTMHEVGHVIG--LVHVFQ-----VSERE 752
Db 360 DFMQQLNGRVLPVNLQIGAKVDYCEBGLKSSASVCLVAGMESLNNSPVCEQI 419
Qy 753 SCNDPCKEYPS-METS-----DLCAD-----773
Db 420 FC--PSPVPLPNGRHTKPLEVPPFGKAVNYTCDPHDRGTSFDLIGESTIRCTSDQGN 477
Qy 774 ---TAPPKSEL--CREPE-----FTSDTCGTRFP--GAPFTYMS 808

```

```

Db 478 GWMSAPRCGILGHCOAPDHFLEPAKLTQTNASDPFGTSLKYECPREYGRBPS----- 533
Qy 809 YTDNCTDNF---TPNOYARHCHLIDLVOQMTESRKPPIPIPPMV----- 852
Db 534 ---ITCDNLWSSPKVCK-----RKSCKTPDPVQMGVHVITDIOGSRIN 578
Qy 853 -----IGQTKSLTI-----HW-LPEI-----SGVYDASGSLGCACTEDGTR 891
Db 579 YSCCTGHRLLGHSAECLISGNAHAWSTKPIQRIQGLPPTIANGDFI-----STNR 632
Qy 892 QYVHTAS--SRRVDSGGYTPREAVGPBDV-----DQCEPSLOAMS--PEVHLVHNM 942
Db 633 ENPHYGVVWYRCKPBGGRKVFELVGPISYCTSNDDQ-----VGIWSGAPQCIIPNK 687
Qy 943 TVPCPTGCSLELLFQHPVQADTTLTWTSFFMSSQVLPFTLELLE---NKSEVHLGPL 999
Db 688 CTRPNV---NGILVSDNRSLSFLNVEVERCOPGFMVMPGR 726
Qy 1000 DTFCDIPLTKLHVDGKVGKVTYTPDEREIDAAALLTSOPHSPLCSG--CRPVRYQVLRD 1058
Db 727 RVKCO-----ALNKMPELPSCSRVCQP----- 749
Qy 1059 PPFASGLPVVYVTHSRKFTDVE--VTPGMYQYQVLAEGSEL--GEAS---PRLNTHGA 1112
Db 750 ---PPOVLAHERTOGRDKDNFSPGOEVYFS--CEPGYDLRGAASRCTPGQDWSPA 800
Qy 1113 PYCG-----DGK---VSERLGEE---CDDGLVSGDGS----- 1140
Db 801 PTCVKSCDDPMGQLNGRVLPVNLQIGAKVFCVCEGQLKSSASVYLAQMESLMN 860
Qy 1141 ---KVCE-----LE-----EGFNCVGPBSL-C 1158
Db 861 SSVPVCEQIFCPBPPIVINGRHGKPLEVFPFGAIVNTCDPHDRKGTSEFGLSESTIRC 920
Qy 1159 YM-YEGDGI-----CE-----PFEKTSIVDCGIYT-----PKGY- 1187
Db 921 TSDPGNGWSSPAPRCGILGHCOAPDHFLEPAKLTQTNASDPFGTSLKYECPREYGR 980
Qy 1188 ---LDQWATRAYSSHED---KKKC--PVSIVTGEPSHLI-----CTSYHPD 1225
Db 981 PFSITCLD---NLWVSSPKDVCKRKSCTPPDPVNGMVHVITDIOGSRINYSCTTGH-R 1036
Qy 1226 LPHNR-----PLTGWFFC-----VASENTODRSQRPESLAKEDV 1263
Db 1037 LIGHSABECILSGNTAMSTKPIQRIQGLPPTIANGDFI--STNR--FNHGSV----- 1090
Qy 1264 WLKVCFRPGEARAF-----IFLITDG-----LVPGHQOQPTT--LYL 1301
Db 1091 -VTRYCMLGSRGRKVFELVGPISYCTSNDDQVIGSGAPQCIIPNKCTPPNVENGILV 1149
Qy 1302 TDVAGSNHSL-----GYGLSCQ-----HNPLIINVTHQNVLF 1336
Db 1150 SD---NRSLSFLNVEVDFRCQPGFMKGPRAVCOALNKMPELPSCSRVCQPPRELH 1205
Qy 1337 --HTTSVLNFSRVRGISAVALTSRIGLSAPSNCTISEDEGONHOGSCITHRCPGQ- 1393
Db 1206 GEHTPSHODNFS---GQEVFYS---EPGYDLGASLSH--CTPPOG 1244
Qy 1394 ---DSCPSLL--LDHADVYVNCSTIGPLMKCAITTCQGFALQASSGQYLRPM 1440
Db 1245 DWSPEARCAVKSDDDELQGLPHGRVLPFLNLQIG-AKVSFVCEBGFRLKSSVSH--- 1299
Qy 1441 QKEILLTCSGSHWDONS--CLPVDGVPDPSSLVYANFSCSEG--TKFLKRCISICVP--- 1495
Db 1300 ---CVLVGMRSILMNSVAVCEHIFCPNP--PALINGRHGTPSGDIPVKEISYTCDDPHD 1355
Qy 1496 ---PAKQGLSPULTCLD---GLMSLPEVYCYL---ECDAPIITIANLILPHCLQ 1543
Db 1356 RGMFTNFIGEST-TRCTSDPHGNGVWSBPAPRCEISVAGHCKTPEOPPFASPTIP--IN 1412
Qy 1544 D-NHNDVGITCKYECKPGYVVAESAEGVRNKLTKIOCLEGIME--GSSCIPVACEPPPP 1600
Db 1413 DFEPPVGTISLNYECPGIF-----GKMFISICLENLWSSVEBDCNRKSCGPPE 1462

```

```

Qy 1601 VFEGM-----YECTNGFSL-----DSQVLANCQEREXPLICTKEGLWTOB 1642
Db 1463 PFNGMVHINIDTORGSTVWVNSCNEGFRLLIGSPSTTCLVSGNNV-----TWDK 1510
Qy 1643 FKLCENLQCEPPPEPSLNS-----VEYKEOGYV----- 1672
Db 1511 APICEII--SCPEPTISNDPFYSNNNTSFHNGTVVYQCHTGPDRQLFELVGERSIYC 1568
Qy 1673 ---IGAVCSP-----LCVTP-SDPVMLENIT---ADTLEHMEP---VKV 1709
Db 1569 TSKDDQVGVWSSPPRCISTNKTCTAPEVENAIRVPGNRSFSLTEILIRFCQPGFVWGS 1628
Qy 1710 QSIYCTGRQWHPDPVLVHCIQSCER 1735
Db 1629 HTVQCQTNGRW--GPKLPHCSRVCP 1652

RESULT 13
5472939-2
Patent No. 5472939
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDIATED DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138, 825
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588, 128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412, 745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332, 865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176, 532
FILING DATE: 01-APR-1988
SEQ ID NO:2
LENGTH: 2039
5472939-2

Query Match 2.9%; Score 287.5; DB 6; Length 2039;
Best Local Similarity 19.1%; Pred. No. 7.7e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

Qy 454 LVLTASFEVNT--BWWP-----RDE-----KYRLEVLQGEPEPELISPLQPL-- 498
Db 34 LALFVANGQCNAPRWLPFAPRNTLTDPEFFIGTYLNECBPGRSGRPFSTICLKNSVWT 93
Qy 499 ---CGQTVCDN-----VELISOYNGWYPRGKVI 525
Db 94 GAKDRCKRKSQRNPDPVNGMVHVYIKIQFGSOIKSCTKGYRLIGSSAIIISGDTVI 153
Qy 526 RYQVNVICD--DEGLNIVSEBOIQLQHEALNEAF---SRYNISWQJSVHOVHNSLRLR 580
Db 154 WDNETPICDRIPCLPPTIT-----NGDFISTNENFHY-----GS 189
Qy 581 VVLVNCERPKIGND-----HCDPECEHPLTYGDG---DCRLQGRCYNNRRDGL 627
Db 190 VVTRYCNPGSGGRKVFELVGPISYCTSNDDQ--VGIWSGAPQCIIPNKCTPPNVENGIL 247
Qy 628 CHVECNMM--LNDPDDDC-----C-----DPOVADVKTCEPDPSPKRAY 666
Db 248 LVSDNRSLSFLNVEVERCQPVFVMKGRPRVYKCOALNKMPELPSCSRVCQPPRELH 306
Qy 667 MSYKELKEALQLNSTHF--LNTYFASVREBDLAGAATW-----PMDKDAVT----- 710
Db 307 ---ERTORDNDNFSPGQEVFYSCEPGYDLRGAASRCTPGQDWSPAPRCEVKSCD 359
Qy 711 ---HLGIVLSAYVYGMGHDTMTLHEVGHVLG---LVHVFYG-----VSERE 752

```

```

Db      360 DFMQGLNGRVLFPVNIQAKAVDFVCDGFLKGSASAYCVLAGMSLWMSVAVCEQI 419
Qy      753 SCNDPKCETVPS -METG----- -DLCAD----- 773
Db      420 FC--PSPPVLPNGHHTGKPLEVPPFGKAVNYTCDPHDRGTSPFLIGSTIRCTSDPOG 477
Qy      774 ---TAPPKSEL---CREPR----- -PTSDTCGTRFP--GAFPTWMS 808
Db      478 GWSMSPARCGIILGHCOAPDHFLFAKLTQTNASDPFISLKTKECPREYGRFSS----- 533
Qy      809 YTTDNCTDNF--TPNOYARMHCYLDLVYQQTESRKETPIPIPPMV----- 852
Db      534 ---ITCIDNLVWSSPKVYCK----- -RKSCTPPDPVAGWVHVIDIOVGRIN 578
Qy      853 -----IGQTKSLTI-----HW--LrPI-----SGVYVDRASGSLGACTEDGTR 891
Db      579 YSCTTGHRLIGHSSAECILSGNAAMWSTKPIICQIPCGLPPTIANGDFI-----STNR 632
Qy      892 QYVHTAS--SRHVCDSGYWTPREAVGPPDV-----DQCEPSILOAMS--PEVHLYHMM 942
Db      633 ENFHYGSVWYTRCNPGRSGKRVFELVGBPSIYCTSNDDQ-----VGIWSGAPQCIIPNK 687
Qy      943 TVPCPTGCSIELLIFQHPVQADTLTWTSPFMSSOVLFPTEILLE--NKESVHIGPL 999
Db      688 CTPEVNE-----NGILVSDNLSFLSNLWVERRCOPGCVMKGPR 726
Qy      1000 DTFCDIPITIKLHVDGKVSQVYTPDERIIDAALLTSCPHSPLCSG--CRVAVYQVLRD 1058
Db      727 RVKCO-----ALNKMBELPSCSKVCP----- 749
Qy      1059 PPFASGLPVVYTHSHRKFTDVE--VTPGQMYQYQVLAEGEL--SEAS-----PPLNHTIGA 1112
Db      750 -----PRDVLHERQORDKONSPGQEVYVS--CEGCVYDLRGAASRCCTPOGDWSPA 800
Qy      1113 PYCG-----DGK--VSERLGEE--CDDGDIVSGDCS----- 1140
Db      801 PTCFVKSQCDPMQGLNGRVLFPVNLQAKAVDFVCDGFLKGSASAYCVLAGMSLW 860
Qy      1141 ---KVCE-----LE-----EGFHCVGBPSL-C 1158
Db      861 SSVAVCQDIFCSPBPVLPNGHHTGKPLEVPPFGKAVNYTCDPHDRGTSPFLIGSESTIRC 920
Qy      1159 YM-VEGDGI-----CE-----PEFKTSIVDCGIYT-----PKGY-- 1187
Db      921 TSDQSGKWSMSPARCGIILGHCOAPDHFLFAKLTQTNADPFISLKTKECPREYGR 980
Qy      1188 ---LDQWATRAYSHED--KKKC--PVSLVTGEPHSLI-----CTSYHPD 1225
Db      981 PFSITCLD--NLVWSSPKDVCKRKSCTPPDPVAGWVHVIDIOVGRINYSCTTGH-R 1036
Qy      1226 LPMNR-----PLTGWPPC-----VASENETODDRSQPBGSLKKEDEV 1263
Db      1037 LIGHSSAECILSGNTAMWSTKPIICQIPCGLPPTIANGDFISTNRENFHYGSV----- 1090
Qy      1264 WLKVCNFRPGBARAIF-----IFLTFDG-----LVPGHQOQPTV--LYL 1301
Db      1091 -VYTRCNLIGSGKRVFELVGBPSIYCTSNDDQVGIWSGAPQCIIPNKCTPPNVENGILV 1149
Qy      1302 TDVGSNHSI-----GYVGLSCQ-----HNPLIINTVTHQONVLEH 1336
Db      1150 SD-----NRSFLSLNEVUDFRCOPGFVMKGPRRVKCOALNKMBELPSCSRVCOPEPTEIH 1205
Qy      1337 --HTTSVLINSSPRAVGISAVALKRTSRIGISABSNCISSEBEGNHQOQSCIHRCGQ-- 1393
Db      1206 GEHTPSHODNESP-----GQEVFVSC--EPGYDLRMAAIAH--CTPQO 1244
Qy      1394 -----DSCPSIL--LDHADVYVCTSIGPGIMCAITCORGFALDSSGGQYIRPM 1440
Db      1245 DWSGPAPRCAYKSCDDFLGOLPHGRVLPPLNDQCS-AKVSFVCDGEGFLKSSSVSH----- 1299
Qy      1441 QKEILLTCSGHWQDNVS--CLPVDCGVDPSPSLVNYANPSCSEG--TKPLKRSISICVP-- 1495
Db      1300 ---CVLVGMRSLMNSVAVCEHIFCPNB--PALINGRHGTSPSGDIPYCKEISYTCDDPHD 1355

```

```

Qy      1496 ---PAKLOGLSPWLTCLED-----GLWSLPEVYCKL-----ECDAPPIILNANILLPHCLO 1543
Db      1356 RGMTEFNLIIGEST--IRCTSDHNGWMSSPAPRCBELSVRACHKCTPBOGFAPASPTIP--IN 1412
Qy      1544 D-NHDVCTICKYECKPQGYIYAESAEGKVRNKLKIQCLBEGIME--QGSCLPVYCEPPPP 1600
Db      1413 DFEFPVGTSLNYECRPGYF-----GKMPSISCLNEMVWSSVDNCRKRS CGPPE 1462
Qy      1601 VFEGM-----YECTNGFSL-----DSQCLVNCQERKLPILCTKEGLWTQE 1642
Db      1463 PFMGMHINTDTPQGSVWVYSCNGBFRLIGSPSTTCLVSGNNV-----TMDK 1510
Qy      1643 FKLCENLQEGCPPPEPSLNS-----VEYKCEQGYG----- 1672
Db      1511 APICEII--SCPEPTISNDDFYSNNRTSPFHNGTVVYQCHGTGPDGQELFELVGBERSIYC 1568
Qy      1673 -----IGAVCSP-----LCYIP-SDPVHLPEHIT--ADTLEHMMER--YKV 1709
Db      1569 TSKXDQVGWSSPPRCISTNKKCTAPEVENAIRVGNRSFPSLTELIRFCQPGFVWGS 1628
Qy      1710 QSIYCTGRQWHPDPLVHGIQSCPE 1735
Db      1629 HTVQOQTNGRM--GPKLPHCSRVCP 1652

RESULT 14
5256642-2
Patent No. 5256642
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES / SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CR1) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO:2:
LENGTH: 2039
5256642-2

Query Match      2.9%; Score 287.5; DB 6; Length 2039;
Best Local Similarity 19.1%; Pred. No. 7.7e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

Qy      454 LVLTASFEPVNT-EMVVF-----RDE-----KYRPLEVYLQGEPPPEILSLQPL- 498
Db      34 LALPVAMGQCNAPWELFAPARTULTDEFEFPPIGYLVYECRPGYSGRPSIILCKNSVMT 93
Qy      499 -----CGQTYCDN-----VELISQYNGWPLRGEKVI 525
Db      94 GAKDRCCRRKSCRNPPDPVNGWVHVIKGIQFSGQIKYSGCTKGYRLIGSSATCIISGDTVI 153
Qy      526 RYQVYVNICD--DESLNIVSEBOQLRQHEALNEAF--SRYNISWQSLVHQVHNSLTLNR 580
Db      154 WNETPPICDRIPCGLPPTIT-----NGDFISTNRENFHY-----GS 189
Qy      581 VLVVNCSPSKIAND-----HCDPESGHPLTGYDG--DCRLQGRCYSMNRDGL 627
Db      190 VYTRCNLIGSGKRVFELVGBPSIYCTSNDDQ--VGIWSGAPQCIIPNKCTPPNVENGILV 247
Qy      628 CHEVCNNM--LNDPDDGDC-----C-----DPQVADVKTCTDPPSPKRAY 666
Db      248 LVSDNRSLSFLNEVVERCQPFVFMKGPBRVVKCOALNKMBELPSCSRVCOPEPTEIHLA- 306

```

```

QY 667 MSVKELEKALQNLNTHF---LNIYFASVREDLAGAATM-----PMDKAVT----- 710
Db 307 -----ERTQORDKNFSPGQEVFPYSCPEGYDLRGAASMRCTPGQDWSPPAAPTCEVNSCD 359
QY 711 -----HIGGIYLSAAYVGMFGHTDTMIHEVHVLG---LYHVFGK-----VSERE 752
Db 360 DFMQQLNGRLVLFVNIQLGAKVDFVCDGQLKSSASYCVLAGMESLWMSVPEQI 419
QY 753 SCNDPCKEYVS-METG-----DLCAD----- 773
Db 420 FC--PSPVLPNGRHTGKPLEVPPFGKAVNYTCDPHPDRGTFDLIGSTRICSTDQGN 477
QY 774 ---TAPRPSKSL---CREPE-----PISDTGCTRRP---GAPFTYMS 808
Db 478 GWSMSPARCGILGHCAPDHFLPAKLTQTNASDPFGTSLKCEPEYVGRBPS----- 533
QY 809 YTDNCTDNF---TPNOVARMHCVLDLYVQWTSRKPPIPIPPV----- 852
Db 534 ---ITCLDNLVWSSPKDYCK-----RKSCTPPDPVGMVHTIDIQVGRIN 578
QY 853 -----IGQTNKSLTI---HW-LRPI-----SGVYDRAAGSLGACTEDGTFR 891
Db 579 YSCTGHRILGHSSABECLISGNAAMWSTKPIQRIQGLPPTIANGDFI-----STNR 632
QY 892 QYVHTAS--SRVCDSSGYTPEBAVGPDPV-----DQCEPGLQANS-PEVHLYHMM 942
Db 633 ENFYGSAVWYTRCNPFGSGRKVFELVGEPSIYCTSNDDQ---VGIWSGAPQCIIPNK 687
QY 943 TVPCPTGCSLELLEFQHVQADTLTLWYTSFMESSQVLPDTLELLE---NKESVHLGPL 999
Db 688 CTRPWE-----NGILVSDNBSLFSLANEVEPRCOPGVVMKGR 726
QY 1000 DTFCDILITKLAVDGRVSGVYTFDERLEIDAALLTQSPHSLCSG-CRPVRYOVLRD 1058
Db 727 RVKCO-----ALNKWEBELPSCSRVCQ----- 749
QY 1059 PPRASGLPVVYTHSHRKTQVYV-VPQGMTOYQVLAEGSL-GEAS---PRLNHIHGA 1112
Db 750 -----PRDLAERTQORDKNFSPGQEVFYS---CEGXYLRKAASRCTPGQDWSPPA 800
QY 1113 PYCG-----DQK---VSERLGEE---CDQGDVLVSGDGS----- 1140
Db 801 PTCGVKSCDDPMQGLNGRLVFPVNLQIGAKVDFVCDGFLKSSASYCVLAGMESLW 860
QY 1141 ---KYCE-----LE-----EGFNCVGEPSL-C 1158
Db 861 SSVAVCEQIFCSPRPVLPNGRHTGKPLEVPPFGKAVNYTCDPHPDRGTFDLIGESTIRC 920
QY 1159 YM-YEGQI-----CE-----PEPKTSIYDCGITY-----PKGY- 1187
Db 921 TSDQGGVWSSPPARCGILGHCAPDHFLPAKLTQTNASDPFGTSLKCEPEYVGR 980
QY 1188 -----LDQWATRAYSSHED---KKKC---PVSIVTGEPSLI-----CTSYHPD 1225
Db 981 PFSITCID--NLVWSSPKDYCKRKSCTPPDPVGMVHTIDIQVGRINYSCTTGH-R 1036
QY 1226 LPHNR-----PLTGWFPCC-----VASENETQDRSEBPESLKKEDV 1263
Db 1037 LIGHSABECLISGNTAMWSTKPIQRIQGLPPTIANGDFISTNRNEMFHVGSV----- 1090
QY 1264 WLKVCNRPGEARAIIF-----IFLTIDG-----LVGEGHQOPTYT--LYL 1301
Db 1091 -VTRCNIGSRGRKVFELVGEPSIYCTSNDDQVIGWSGPAPQCIIPNKCTPPNENGILV 1149
QY 1302 TDVAGSNHSL-----GTGSLSCQ-----HNPLINTVTHHQNVLFI 1336
Db 1150 SD-----NBSLFSLANEVDRCOPGVVMKGRPVKVCQALNKWERPELPSGSRVCOQRPPELTH 1205
QY 1337 --HTSVLANFSSBRVVISAVALTSSRIGLSABNSCISDEGQNHQOQSCIHRRPCGQ- 1393
Db 1206 GEHTPSHQDNFSP-----GQEVFVSC---EPGYDLRGAASLTH--CTPQG 1244

```

```

QY 1394 -----DSCPSLL--LDHADVVNCTSIGPGLMKCAITCORGFALQASSGQYIRPM 1440
Db 1245 DWSPEARCAVKSDDPLGQLPHGRVLPFLNLQIG-AKVSFVCDGRLKSSVSH----- 1299
QY 1441 QKEILLTSSGSHMDQVNS-CLPYDCGVDPBSLVNVAWNSGSEG-TKFLKXCSISCV- 1495
Db 1300-----CVLVGMRSLWMSNV/PVCEBHIFCPNP-FALINGRHTGTPSGDIPYGEKISYTCDBHPD 1355
QY 1496 ---PAKIQGLSPWLTCLD---GLASLPEVYCYL-----ECDAPIITIANLILPHCLO 1543
Db 1356 RGMTEFNIGEST-IRCTSDPHGNGWSSPPARCELSVRAHGCKTPEQFPFAISPTIF-IN 1412
QY 1544 D-NHDVGTICKYCKECPGYUVAASABGKVRKLLKIOCLEGIME--QOCSIPVCEPPPP 1600
Db 1413 DPEFPVGTSLNYECPGIF-----GKMSISCLLENLWMSVEDNCKRKSQGPPE 1462
QY 1601 VFEGM-----YECTNGFSL-----DSQVLANQREKPLICTKESGLWTOE 1642
Db 1463 PFNGMVHINTDQGSTVNVSCNNGFRLIGSPSTTCLVSGNV-----TWDK 1510
QY 1643 FKLCENIQGBCPPPSFLNS-----VEYKCEQYG----- 1672
Db 1511 APICEII--SCBEPPTISNGDFYSNNRTSFHNGTVVYQCHTGPDBGOLPELVGERSIYC 1568
QY 1673 ---IGAVCSP-----LCVIRP-SDPYMLPENIT---ADTLEHMMEP-----YKV 1709
Db 1569 TSKDDQGVWSSPEPRCISTNKTCTAPEVENAIRVGNRSFPSTLTETIRFCQPGFVWGS 1628
QY 1710 QSIIVCTGRQWHPDPLVWLCIQSCEP 1735
Db 1629 HTVQCGQJNGRW--GPKLPHCSRVQCP 1652

RESULT 15
5472939-2
Patent No. 5472939
Applicant: PEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
MEDIATED DISORDERS
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/138,825
FILING DATE: 19-OCT-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 588,128
FILING DATE: 24-SEP-1990
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO:2
LENGTH: 2039
5472939-2

Query Match 2.9%; Score 287.5; DB 6; Length 2039;
Best Local Similarity 19.1%; Pred. No. 7.7e-15;
Matches 349; Conservative 176; Mismatches 548; Indels 751; Gaps 105;

QY 454 LVLTASFEPVNT-EWVPF-----RDF-----KYPLEVLQGFEPPELISPLQPPV- 498
Db 34 LALPVANGQCNAPBWLFPARPTNLTDBFEPPIGYLVYECGPGYSGRPSIICLKNSVMT 93
QY 499 ---CGQYCDN-----VELISQYNGWPRGRGKY 525
Db 94 GAKDRCKRKSCKRPPDPVNGMVHVIKIQGSGQIKYISCTGYRLIGSSSATCIIISGDIY 153
QY 526 RYQVNVICD--DEGLNPIVSEBOQRIQHEALNBAF--SRVNISSWQLSVHQVHNSLRR 580
Db 154 WDNETPICDRIQGLPPTIT-----NGDFISTNNENFHY-----GS 189

```

```

Qy 581 VVLVNCPEPSKIGND-----HCDPECEHPLTGDG--DCLQGRCSYWNRRDGL 627
Db 190 VVTRCPCPGSGGRVFLVGPSPSYCTSNDDQ--VGIWSPAPCCIIIPNKCTPPNVNGI 247
Qy 628 CHVECNMM--LNDPDDGDC-----C-----DPOVAVKTCFDPDPSPRAY 666
Db 248 LVSNDRLSFLINVEVEFCQCFVFWKGRPRVYCOALNKMWBELSPCSRVCQPPDVLHA- 306
Qy 667 MSVVELKEALQNSTHF--LNIYFASVREDLAGAATW-----PMDKAVT----- 710
Db 307 -----ERTORDXDNFSPQGEVYFSCPEGYDLGASMRCTPGQDMSPAAPTECVASCD 359
Qy 711 -----HIGIIVLSPAYGMPGHTDTMLHVGHLV--LYHVFGR-----VSERE 752
Db 360 DFMQQLNGRVLFVYVNIQLGAKVDFVCDGFOLGSSASYCVLAGMESLWMSVPCEQI 419
Qy 753 SCNDPCKETVPS--METG-----DLCAD----- 773
Db 420 FC--PSPVLIENGHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGSTIRCTSDPQGN 477
Qy 774 ---TAFTPKSEL--CREPE-----PISDTGCTRP--GAFTYMS 808
Db 478 GWSPPAPRCGILGHCAPDHFLPAKLQTNASDFPIGTSLKXECREYVGRPS--- 533
Qy 809 YTDNCTDNF---TPNOVARMHGCLDLVYQOWTESRKPTPIPIPMV----- 852
Db 534 ---ITCDNLVWSSPKDYCK-----RKSCTPPDPVAGMHVITDIOVGRIN 578
Qy 853 -----IGOTNKSLLT---HW--LPI---SGVYDRASSGLSCAGTEDGTFR 891
Db 579 YSCTTGRLHIGSSAECILSGNAHWSKPIQRIPIGCLPPTLANGDFI-----STNR 632
Qy 892 QYVHTAS--SKRVCDSSGYTWPEBAVGPV--DQPCERBLQMS--PEVHLHYMM 942
Db 633 ENFHYGAVVYTRCNPGSGGRVFLVGPSPSYCTSNDDQ--VGIWSPAPCCIIIPNK 687
Qy 943 TVPCPTGCSLELLFQHPVQADTLTLWTSFFMESSQVLPTEILL--NKESVHLGPL 999
Db 688 CTRPNVE-----NGILVSDNRSLFSLNVEVERCOQPGFVMGPR 726
Qy 1000 DTFCDIPLTLKLVADGKVSQVYTFPDERIIDAALLTSQHPSPCSG--CRPVRYQVLRD 1058
Db 727 RVKCO--ALNKMWBELSPCSRVCQ----- 749
Qy 1059 PPFASGLPVVYTHSHRKTVE--VTRQMYQYVLAEGSL--GRAS-----PPLNHIGA 1112
Db 750 -----PPDLHAERTQORDXDNFSPQGEVYF--CEPGYDLRGASMRCTPGQDMSPA 800
Qy 1113 PYCG-----DGK--VSERLGEE---CDGDLVSGDGS----- 1140
Db 801 PTCVKSCDDEFMQGLNRLVLPVNIQLGAKVDFVCDGFOLGSSASYCVLAGMESLWN 860
Qy 1141 --KVCE-----LE-----EGFNCVGPBSL-C 1158
Db 861 SSVVPCEQIFCPSPVLPNGRHTGKPLEVFPFGKAVNYTCDPHPDRGTSFDLIGESTIRC 920
Qy 1159 YM-VEGDI-----CR-----PEPKTSIVDCGIYT-----PKGY-- 1187
Db 921 TSDPQNGWSSPAPRCGILGHCAPDHFLPAKLQTNASDFPIGTSLKXECREYVGR 980
Qy 1188 -----LDQWATRAYSHED--KKKC--PVSIVTGEPSHLI-----CTSYPHD 1225
Db 981 PFSITCUD--NLWSSPKDYCKRSKCTPPDPVNGMHVITDIOVGRINYSCTTGH-R 1036
Qy 1266 LPHNR-----PLTGWPC-----VASENETQDRSEQPEGLKKEDEV 1263
Db 1037 LIGHSASECILSGNTAHWSTKPIQRIPIGCLPPTLANGDFISTNRENFHYGSV----- 1090
Qy 1264 WLKTCFNRPGARAF-----IFLTIDG-----LVPGHQOPTYT--LYL 1301
Db 1091 -VYTRCNLGRGRKRVFLVGPSPSYCTSNDDQVGIWSPAPCCIIIPNKCTPPNVNGILV 1149

```

```

Qy 1302 TDVGRNSHL-----GTYLSCQ-----HNPILIIVTHQNVLFH 1336
Db 1150 SD-----NRSLFSLINEVDFRCQPFVWKGPRRYVCOALNKMWBELSPCSRVCQPPPEILH 1205
Qy 1337 -HTTSLVLFSSPRVGISVALRTSSRIGLSAPSNQISBDEQNHQGOSCHRPCQKO- 1393
Db 1206 GEHTPSHQDNFSP-----GOEYFSC--EPGIDLGASLH--CTPQG 1244
Qy 1394 -----DSCPSLL--LDHADVYVNTSIGFGMLKCAITCQRFALQASSGQYIRPM 1440
Db 1245 DMSPEAPRCAYKSCDDPLGQLPHGRVLPPLNIQLG-AKVSFVDEGRFLKSSVSH----- 1299
Qy 1441 QKEILLTCSSGHWQVNS--CLPVDCGVDPDLVNYANFSCSEG--TKFLKCSISCV- 1495
Db 1300 ---CVLWGRMSLWNNNSVPVCEHIFCPNP--PAILNGRHTGPSGDIPIYKKEISYCDHPD 1355
Qy 1496 ---PAKLGSPMLTLED---GLMSLEPVYCKL-----ECAPPIILNANLLPHCLO 1543
Db 1356 RGMTFNLIGEST-IRCTSDPHGNGWSSPAPRCGLSVRAGHCKTPEQPPASPTIP--IN 1412
Qy 1544 D-NHDVGTICKYCKPGYVVAESAEGKVRNKLKIOCLEGGIWE--QGSCLPVVCEBPPP 1600
Db 1413 DFERPVGTSINYECPGF-----GKMSISICLENLWMSVVDNCRKSCGPPE 1462
Qy 1601 VFEQM-----YECTNGFSL--DSQVLANQOBEREKLPICTKEGLMTQOE 1642
Db 1463 PFNGMVHINTDQFGSTVYNSCNEGFRILGSPSTYCLVSGNNV-----TWDXK 1510
Qy 1643 FKUCENLQGRCPPPPSLNS-----VEYKQEOGYG----- 1672
Db 1511 APICEII--SCEPPTISNGDFYSNNRTSFHNGTIVVYQCHTGDEQLFELVGENSIYC 1568
Qy 1673 -----IGAVCSP-----LCVIRP--SDPVMLENIT-----ADTLEHMMER--VKV 1709
Db 1569 TSKDDQYGVWSSPPRPICSTINKCTAPREVENAIVPGRSPFSLTEILIRPQCPGFVWGS 1628
Qy 1710 QSIIVCTGRQWHPDVLVHCIOQCEP 1735
Db 1629 HTVQCOTNGRW--GPKLPHCSRVCOF 1652

```

Search completed: August 25, 2005, 22:25:38
 Job time : 53.4828 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 22:20:01 ; Search time 127.279 Seconds

(without alignments)
5529.033 Million cell updates/sec

Title: US-09-983-025B-2

Perfect score: 9856

Sequence: 1 MWGLKIRISLAILAGWALC.....AADCDLDECTCRPKAEENG 1791

Scoring table: BLOSUM62

Gapop 10.0 , Gapect 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database :	Published Applications AA:*
1:	/cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
2:	/cgn2_6/ptodata/2/pubppaa/PCT_NEW_PUB.pep.*
3:	/cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
4:	/cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
5:	/cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
6:	/cgn2_6/ptodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
7:	/cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
8:	/cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
9:	/cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
10:	/cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
11:	/cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
12:	/cgn2_6/ptodata/2/pubppaa/US09_NEW_PUB.pep.*
13:	/cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
14:	/cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
15:	/cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
16:	/cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
17:	/cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep.*
18:	/cgn2_6/ptodata/2/pubppaa/US10F_PUBCOMB.pep.*
19:	/cgn2_6/ptodata/2/pubppaa/US10G_PUBCOMB.pep.*
20:	/cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
21:	/cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
22:	/cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	9856	100.0	1791	10	US-09-983-025-2
2	9836	99.8	1791	9	US-09-827-998-3
3	9836	99.8	1791	15	US-10-675-685-3
4	9507	96.5	1770	9	US-09-827-998-10
5	9507	96.5	1770	15	US-10-675-685-10
6	7363	74.7	1385	9	US-09-827-998-16
7	7363	74.7	1385	15	US-10-675-685-16
8	3916.5	39.7	1627	10	US-09-983-025-25
9	3916.5	39.7	1627	15	US-10-295-027-663
10	3916.5	39.7	1627	17	US-10-783-311-1
11	3916.5	39.7	1627	17	US-10-741-600-1406

12	3916.5	39.7	1627	17	US-10-991-321-32	Sequence 32, App1
13	3916.5	39.7	1627	18	US-10-887-229A-8	Sequence 8, App1
14	3914.5	39.7	1547	17	US-10-783-311-2	Sequence 2, App1
15	3602	36.5	1420	17	US-10-741-600-1403	Sequence 1403, App
16	3602	36.5	1420	17	US-10-741-600-1405	Sequence 1405, App
17	3044	30.9	1232	17	US-10-741-600-1404	Sequence 1404, App
18	2219	22.5	858	15	US-10-334-143-85	Sequence 85, App1
19	1893	19.2	704	17	US-10-741-600-1402	Sequence 1402, App
20	1086	11.0	192	9	US-09-864-761-34255	Sequence 34265, A
21	383	3.9	70	9	US-09-864-761-34264	Sequence 34264, A
22	360.5	3.7	165	9	US-09-864-761-42873	Sequence 42873, A
23	346.5	3.5	3567	15	US-10-028-248A-47	Sequence 47, App1
24	346.5	3.5	3567	15	US-10-107-782-47	Sequence 47, App1
25	336.5	3.4	3571	16	US-10-603-283-2	Sequence 2, App1
26	336.5	3.4	3594	13	US-09-911-842-4	Sequence 4, App1
27	336.5	3.4	3594	13	US-10-150-821-4	Sequence 4, App1
28	334.5	3.4	3557	15	US-10-295-027-430	Sequence 430, App
29	334.5	3.4	3557	15	US-10-295-027-1297	Sequence 1297, App
30	332.5	3.4	3568	15	US-10-028-248A-8	Sequence 8, App1
31	332.5	3.4	3568	15	US-10-107-782-8	Sequence 8, App1
32	332.5	3.4	3570	15	US-10-028-248A-6	Sequence 6, App1
33	332.5	3.4	3570	15	US-10-107-782-6	Sequence 6, App1
34	330.5	3.4	3571	13	US-09-911-842-2	Sequence 2, App1
35	330.5	3.4	3571	13	US-10-150-821-2	Sequence 2, App1
36	324	3.3	63	9	US-09-864-761-34262	Sequence 34262, A
37	292.5	3.0	2489	9	US-09-911-842-5	Sequence 5, App1
38	292.5	3.0	2489	13	US-10-150-821-5	Sequence 5, App1
39	292.5	3.0	2489	17	US-10-741-600-1242	Sequence 1242, App
40	290	2.9	3564	15	US-10-016-248-45	Sequence 45, App1
41	287.5	2.9	2039	17	US-10-741-600-1241	Sequence 1241, App
42	287.5	2.9	2044	15	US-10-276-774-2152	Sequence 2152, App
43	287	2.9	1947	16	US-10-742-887-52	Sequence 52, App1
44	283	2.9	1139	9	US-09-764-893-102	Sequence 102, App
45	283	2.9	1139	9	US-09-764-881-99	Sequence 99, App1

ALIGNMENTS

RESULT 1
US-09-983-025-2
Sequence 2, Application US/09983025
Publication No. US20030124529A1
GENERAL INFORMATION:
APPLICANT: OXVIG, Claus
TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)
FILE REFERENCE: OXVIG-1A
CURRENT APPLICATION NUMBER: US/09/983, 025
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/241, 840
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: DK PA 2000 01571
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
FEATURES:
NAME/KEY: misc_feature
LOCATION: (1)..(66)
OTHER INFORMATION: prepro part of PAPP-A2
NAME/KEY: misc_feature
LOCATION: (67)..(699)
OTHER INFORMATION: pro part of PAPP-A2
US-09-983-025-2
Query Match 100.0%; Score 9856; DB 10; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1791; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

Qy 1 MCKLIRISLIALAGMALCSANSELGWTRRKSLVEREHLNQVLEGERCWLGAQVRR 60
Db 1 MMCKLIRISLIALAGMALCSANSELGWTRRKSLVEREHLNQVLEGERCWLGAQVRR 60
Qy 61 ASPQHLLFGVYPSAAGNYLRPYVGEQEIHTHTGSKPDTEGNAVASLVPPDLTENPAGIRG 120
Db 61 ASPQHLLFGVYPSAAGNYLRPYVGEQEIHTHTGSKPDTEGNAVASLVPPDLTENPAGIRG 120
Qy 121 AVEBPAPWVGSDPLIGSELLGDDDAYLGNRSKESLGEAGIQGSAAMAATTTTALFTTL 180
Db 121 AVEBPAPWVGSDPLIGSELLGDDDAYLGNRSKESLGEAGIQGSAAMAATTTTALFTTL 180
Qy 181 NEBPETORRGMAKSRORQVWKRAEDQGDSDGISHFQWPKSLKHRYKSPREESN 240
Db 181 NEBPETORRGMAKSRORQVWKRAEDQGDSDGISHFQWPKSLKHRYKSPREESN 240
Qy 241 QNGEGSYREAFETNSQVGLPILYFSGRERILLRPEVLAEI PREAFTEAMVREBQGN 300
Db 241 QNGEGSYREAFETNSQVGLPILYFSGRERILLRPEVLAEI PREAFTEAMVREBQGN 300
Qy 301 NPALIAGFDCSHTVSDKGMALGIRSGKDKXDPARFPFSLCTDRYKKAATILISHRYQ 360
Db 301 NPALIAGFDCSHTVSDKGMALGIRSGKDKXDPARFPFSLCTDRYKKAATILISHRYQ 360
Qy 361 PGTWTHVAATYDGRHMLLYVDGTQVASSLDQSGPLNSPFMASCSRLILGDSSEGHYFR 420
Db 361 PGTWTHVAATYDGRHMLLYVDGTQVASSLDQSGPLNSPFMASCSRLILGDSSEGHYFR 420
Qy 421 GHLLTLVFWSTALPOSHFOHSSQHSGBEATDVLTLASFEPVTEWVPRDEKXPRLV 480
Db 421 GHLLTLVFWSTALPOSHFOHSSQHSGBEATDVLTLASFEPVTEWVPRDEKXPRLV 480
Qy 481 LQGEPEBELISPLQPLCGQTVCDNVELISQYNGWMLRGEKXIRYOVVNI CDDEGLN 540
Db 481 LQGEPEBELISPLQPLCGQTVCDNVELISQYNGWMLRGEKXIRYOVVNI CDDEGLN 540
Qy 541 IVSEEOIRLOHEALNEAFSRYNISWOLSVHQVHNSLHRVVLVNCBPSKIGNDHCP 600
Db 541 IVSEEOIRLOHEALNEAFSRYNISWOLSVHQVHNSLHRVVLVNCBPSKIGNDHCP 600
Qy 601 EHPILTGIDGDCRLQGRCYSWNRDGLCHECNMMLNFDGDCDDQVADVARTKCEPD 660
Db 601 EHPILTGIDGDCRLQGRCYSWNRDGLCHECNMMLNFDGDCDDQVADVARTKCEPD 660
Qy 661 SPKRAYSVKELKEALQNLNSTHPLNTIYFASVREDLAGAATWPDKXAVHILGGLVSPA 720
Db 661 SPKRAYSVKELKEALQNLNSTHPLNTIYFASVREDLAGAATWPDKXAVHILGGLVSPA 720
Qy 721 YYGMPGHDTMIHEVGHVGLIYHVPKGVSERESCNDECKETVPMETGDLCAOTAPTPKS 780
Db 721 YYGMPGHDTMIHEVGHVGLIYHVPKGVSERESCNDECKETVPMETGDLCAOTAPTPKS 780
Qy 781 ELCEBEPSTDCGFTFPGAPFTNYMSYTDNCTDNFTFNOVARMHCYLDLVYQMTES 840
Db 781 ELCEBEPSTDCGFTFPGAPFTNYMSYTDNCTDNFTFNOVARMHCYLDLVYQMTES 840
Qy 841 RKPRPIIPRVYIGOTKSLTIHLPLISGVYVYRASGSLCGAATBEGTFRQVYHTASSR 900
Db 841 RKPRPIIPRVYIGOTKSLTIHLPLISGVYVYRASGSLCGAATBEGTFRQVYHTASSR 900
Qy 901 RVCDSSGWTPEEAVGPVDVQCEPSIQAMSPEVHLVHMNTVPCPTGEGSELLOHP 960
Db 901 RVCDSSGWTPEEAVGPVDVQCEPSIQAMSPEVHLVHMNTVPCPTGEGSELLOHP 960
Qy 961 VOADTLTLWTSFPMESSQVLFTEILLNKESVHLGPDITCDIPLTIKLHVDGKVS 1020
Db 961 VOADTLTLWTSFPMESSQVLFTEILLNKESVHLGPDITCDIPLTIKLHVDGKVS 1020
Qy 1021 KVVTFEDRIETDALILSOPHSPLCSGCRPVRYOVLADPPASGLPVVYVTHSHRKF 1080
Db 1021 KVVTFEDRIETDALILSOPHSPLCSGCRPVRYOVLADPPASGLPVVYVTHSHRKF 1080
Qy 1081 VTPGOMYQOVLAEAGELGASPLNHIHGAPYCGDGKVSERLGECECDODLVSGDGS 1140

```

```

Db 1081 VTPGOMYQOVLAEAGELGASPLNHIHGAPYCGDGKVSERLGECECDODLVSGDGS 1140
Qy 1141 KVCELEBGFNCVGPSPICYMEBGDICEPFRKTSIYDCGITYPKGLDQWATPAYSHE 1200
Db 1141 KVCELEBGFNCVGPSPICYMEBGDICEPFRKTSIYDCGITYPKGLDQWATPAYSHE 1200
Qy 1201 DKKCPVSLVTGEPHSLICTSYHPDLPHNRPLTCMFVASENETODRSEOPESLKE 1260
Db 1201 DKKCPVSLVTGEPHSLICTSYHPDLPHNRPLTCMFVASENETODRSEOPESLKE 1260
Qy 1261 DEWMLKVCNRPGEARAIFFLTDTGLVPEHQPTVTLVTLTVRGSNHSIGTYGLSCQH 1320
Db 1261 DEWMLKVCNRPGEARAIFFLTDTGLVPEHQPTVTLVTLTVRGSNHSIGTYGLSCQH 1320
Qy 1321 NPLIINTHQNVLPHHTTSVLNFSFPRVIGISVARTSRIGLSAPSNCISEBEOQH 1380
Db 1321 NPLIINTHQNVLPHHTTSVLNFSFPRVIGISVARTSRIGLSAPSNCISEBEOQH 1380
Qy 1381 QGOSCHRPCKODSCPSLLDHDVYNCTSIGGLMKCAITCORGFALQASSGOYIRPM 1440
Db 1381 QGOSCHRPCKODSCPSLLDHDVYNCTSIGGLMKCAITCORGFALQASSGOYIRPM 1440
Qy 1441 QKEILLTCSSGHDQVNSCLPVDGVPDPSLVVYANFSCSEGTKFLKRSISCVPAKLQ 1500
Db 1441 QKEILLTCSSGHDQVNSCLPVDGVPDPSLVVYANFSCSEGTKFLKRSISCVPAKLQ 1500
Qy 1501 GLSPMLTCLBDDGLMSLPBYVCKLECDAPRIILNANLLPHCLDNHNVGTLCKYCEKPGY 1560
Db 1501 GLSPMLTCLBDDGLMSLPBYVCKLECDAPRIILNANLLPHCLDNHNVGTLCKYCEKPGY 1560
Qy 1561 YVASEAGKRYNKLKIQCLEGGIWEQSGCIPVCEBPPPVFEGMYECTNGFSLDSQCVL 1620
Db 1561 YVASEAGKRYNKLKIQCLEGGIWEQSGCIPVCEBPPPVFEGMYECTNGFSLDSQCVL 1620
Qy 1621 NCNQRKPLILCTKEGLMTQEFKLCENLQGECPPEPSELNSVEYKCEGYGIGAVCSPL 1680
Db 1621 NCNQRKPLILCTKEGLMTQEFKLCENLQGECPPEPSELNSVEYKCEGYGIGAVCSPL 1680
Qy 1681 CVTPSPDPMVLPENITADTLLEHMEBPVKQSIYCTGRQHPVPLVHCIOSECPFQADG 1740
Db 1681 CVTPSPDPMVLPENITADTLLEHMEBPVKQSIYCTGRQHPVPLVHCIOSECPFQADG 1740
Qy 1741 WCPTINNRACVHDGDCSSSTLSSKKVIPFAADCDLDECTCADPKAEENO 1791
Db 1741 WCPTINNRACVHDGDCSSSTLSSKKVIPFAADCDLDECTCADPKAEENO 1791

```

RESULT 2

US-09-827-998-3

Sequence 3, Application US/09827998

Patent No. US20020102252A1

GENERAL INFORMATION:

APPLICANT: Gu, Yizhong

TITLE OF INVENTION: Novel ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: MDHMRP-8

CURRENT APPLICATION NUMBER: US/09/827, 998

PRIOR FILING DATE: 2001-04-06

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Aecomica Sequence Listing Engine

SEQ ID NO 3

LENGTH: 1791

TYPE: PRT

ORGANISM: Homo sapiens

US-09-827-998-3

Query Match 99.8%; Score 9836; DB 9; Length 1791;
 Best local Similarity 99.8%; Pred. No. 0;

Matches 1788; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

```

Qy 1 MMCKIIRISLAIAGALCSANSELGWTTRKSLVEREHLNOVLLBEGRCMLGAKVRRP 60
Db 1 MMCKIIRISLAIAGALCSANSELGWTTRKSLVEREHLNOVLLBEGRCMLGAKVRRP 60
Qy 61 ASPQHLFGVPSRAGVLRPYVGEQIHHHTGSKPDTEGNAVSLVPPDLTENPAGLRG 120
Db 61 ASPQHLFGVPSRAGVLRPYVGEQIHHHTGSKPDTEGNAVSLVPPDLTENPAGLRG 120
Qy 121 AVEBPAAFWGDSPIQSGELLGDDAYLGNQSKESLGBAGIQGSAAMAATTITAIPTTL 180
Db 121 AVEBPAAFWGDSPIQSGELLGDDAYLGNQSKESLGBAGIQGSAAMAATTITAIPTTL 180
Qy 121 AVEBPAAFWGDSPIQSGELLGDDAYLGNQSKESLGBAGIQGSAAMAATTITAIPTTL 180
Db 121 AVEBPAAFWGDSPIQSGELLGDDAYLGNQSKESLGBAGIQGSAAMAATTITAIPTTL 180
Qy 181 NEPEPEQRGMASRQROQWKRABDQDQSGISHPQWPKSLKHKRKSPPESN 240
Db 181 NEPEPEQRGMASRQROQWKRABDQDQSGISHPQWPKSLKHKRKSPPESN 240
Qy 181 NEPEPEQRGMASRQROQWKRABDQDQSGISHPQWPKSLKHKRKSPPESN 240
Db 181 NEPEPEQRGMASRQROQWKRABDQDQSGISHPQWPKSLKHKRKSPPESN 240
Qy 241 QNGEGSYREATNSOVGLPIFYSGRRELLRPEVLAETPREAFTVEAMVREGON 300
Db 241 QNGEGSYREATNSOVGLPIFYSGRRELLRPEVLAETPREAFTVEAMVREGON 300
Qy 241 QNGEGSYREATNSOVGLPIFYSGRRELLRPEVLAETPREAFTVEAMVREGON 300
Db 241 QNGEGSYREATNSOVGLPIFYSGRRELLRPEVLAETPREAFTVEAMVREGON 300
Qy 301 NPALIAVFDNCSHTVSDKGMALGIRSGKDKRDAEFPSLCTDRVKKATILISHRYQ 360
Db 301 NPALIAVFDNCSHTVSDKGMALGIRSGKDKRDAEFPSLCTDRVKKATILISHRYQ 360
Qy 301 NPALIAVFDNCSHTVSDKGMALGIRSGKDKRDAEFPSLCTDRVKKATILISHRYQ 360
Db 301 NPALIAVFDNCSHTVSDKGMALGIRSGKDKRDAEFPSLCTDRVKKATILISHRYQ 360
Qy 361 PGWTHVAATYDGNHMLLYDGTQVASSLDQSGPLNSPMASSCSLLIGDSSSDGHYFR 420
Db 361 PGWTHVAATYDGNHMLLYDGTQVASSLDQSGPLNSPMASSCSLLIGDSSSDGHYFR 420
Qy 421 GHIGTLFWSTALQSHFQSHSSGSEBEATDLVLTASPEPVNTWMPPEDEKYPLEV 480
Db 421 GHIGTLFWSTALQSHFQSHSSGSEBEATDLVLTASPEPVNTWMPPEDEKYPLEV 480
Qy 481 LOGEPEPELISPLQPLCGQTVCDNVELISQYNGYMPLRGEKIRYQVNNICDEGLNP 540
Db 481 LOGEPEPELISPLQPLCGQTVCDNVELISQYNGYMPLRGEKIRYQVNNICDEGLNP 540
Qy 481 LOGEPEPELISPLQPLCGQTVCDNVELISQYNGYMPLRGEKIRYQVNNICDEGLNP 540
Db 481 LOGEPEPELISPLQPLCGQTVCDNVELISQYNGYMPLRGEKIRYQVNNICDEGLNP 540
Qy 541 IVSEBQIRLOHEALNEAFSRYNISWOLSVHOVNSTLRHVLYVNCBPSKTDNDCHDEC 600
Db 541 IVSEBQIRLOHEALNEAFSRYNISWOLSVHOVNSTLRHVLYVNCBPSKTDNDCHDEC 600
Qy 541 IVSEBQIRLOHEALNEAFSRYNISWOLSVHOVNSTLRHVLYVNCBPSKTDNDCHDEC 600
Db 541 IVSEBQIRLOHEALNEAFSRYNISWOLSVHOVNSTLRHVLYVNCBPSKTDNDCHDEC 600
Qy 601 EHPITGVDGDCRLOGRCYSNNRRDGLCHVCCNNMLNDFDGDCCDQVAVRKTCPED 660
Db 601 EHPITGVDGDCRLOGRCYSNNRRDGLCHVCCNNMLNDFDGDCCDQVAVRKTCPED 660
Qy 661 SPKRAVSVKELKALQNSTHFLNIYFASVREDLAGAATPWMDKXAVTHLGIVLSPA 720
Db 661 SPKRAVSVKELKALQNSTHFLNIYFASVREDLAGAATPWMDKXAVTHLGIVLSPA 720
Qy 721 YGMPGHDTMIEHGVHLGLYHVFKGVSERESCNDPCKETVPSMETGDLCAATAPTPKS 780
Db 721 YGMPGHDTMIEHGVHLGLYHVFKGVSERESCNDPCKETVPSMETGDLCAATAPTPKS 780
Qy 721 YGMPGHDTMIEHGVHLGLYHVFKGVSERESCNDPCKETVPSMETGDLCAATAPTPKS 780
Db 721 YGMPGHDTMIEHGVHLGLYHVFKGVSERESCNDPCKETVPSMETGDLCAATAPTPKS 780
Qy 781 ELCREPEPTSDTCGTFRPGAPFTNMSYTDNDCTDNTPTPOVARMCIYDLVYQWTES 840
Db 781 ELCREPEPTSDTCGTFRPGAPFTNMSYTDNDCTDNTPTPOVARMCIYDLVYQWTES 840
Qy 841 RKPTPIIPMVVIGQTKSLTIHMLPRTSGVYDRASSGLCGATEBGTFRQYVHTASSR 900
Db 841 RKPTPIIPMVVIGQTKSLTIHMLPRTSGVYDRASSGLCGATEBGTFRQYVHTASSR 900
Qy 901 RVCSSSGYMTPEEAVGPVDVQCEPSIQAMSPEVHLVHMMNTVPCTEGCSLELLFQHP 960
Db 901 RVCSSSGYMTPEEAVGPVDVQCEPSIQAMSPEVHLVHMMNTVPCTEGCSLELLFQHP 960
Qy 961 VQADTLTLMWTSFMESQVLFDEIILLENKESVHLGPDFFCDIPLTIKLVHNGKXSV 1020
Db 961 VQADTLTLMWTSFMESQVLFDEIILLENKESVHLGPDFFCDIPLTIKLVHNGKXSV 1020
Qy 1021 KVTYFDERIEIDALITSPHSPICSGCRPVRYOVULDPFPASGLPVVVTSHHKKFTDVE 1080
Db 1021 KVTYFDERIEIDALITSPHSPICSGCRPVRYOVULDPFPASGLPVVVTSHHKKFTDVE 1080

```

```

Qy 1081 VTPGOMYOYUABAGELGASPLNHIHGAPYCGPKVSERLGBECDDGLVSGDGS 1140
Db 1081 VTPGOMYOYUABAGELGASPLNHIHGAPYCGPKVSERLGBECDDGLVSGDGS 1140
Qy 1141 KVCELEBGFNCVGPSPCLMYMEGDGICEPPEKRTSIVDCGIYTPKGYLDQWATRASHE 1200
Db 1141 KVCELEBGFNCVGPSPCLMYMEGDGICEPPEKRTSIVDCGIYTPKGYLDQWATRASHE 1200
Qy 1201 DKKKCPVSLVTGEPHSLICTSYAPDLFNNRPLTGMFCVASENRTODDRSQPEGLKKE 1260
Db 1201 DKKKCPVSLVTGEPHSLICTSYAPDLFNNRPLTGMFCVASENRTODDRSQPEGLKKE 1260
Qy 1261 DEWVLKVCENRPGBARAIFLITTDGLVPGHQOPTYTLVTVDRGSNHSIGTGSLCQH 1320
Db 1261 DEWVLKVCENRPGBARAIFLITTDGLVPGHQOPTYTLVTVDRGSNHSIGTGSLCQH 1320
Qy 1321 NPLIINTVHHQNVLFHHTTGYLNFSSPRVGISAVALRTSRIGLSAPNSCISEDEGON 1380
Db 1321 NPLIINTVHHQNVLFHHTTGYLNFSSPRVGISAVALRTSRIGLSAPNSCISEDEGON 1380
Qy 1381 QGSCIRPCGKODSCPSLLIDHADVNVCTSIGGLMKCAITCORGALQASSGOYIRPM 1440
Db 1381 QGSCIRPCGKODSCPSLLIDHADVNVCTSIGGLMKCAITCORGALQASSGOYIRPM 1440
Qy 1441 QKEITLTCSSGHDQNVSCIPVDCGVPDPBSLVNANFSCSRTGFKRCSISCVPAKQ 1500
Db 1441 QKEITLTCSSGHDQNVSCIPVDCGVPDPBSLVNANFSCSRTGFKRCSISCVPAKQ 1500
Qy 1501 GLSPMLTCLBEGDLSPEVYCKLECDAPITLNNLLPHCLQDNHVDGTICKYCKRGY 1560
Db 1501 GLSPMLTCLBEGDLSPEVYCKLECDAPITLNNLLPHCLQDNHVDGTICKYCKRGY 1560
Qy 1561 YVASAGKVRNKLKIQCLEGIMEQSCIPVCEPPPVPEGMYECTNFSLDSQCVL 1620
Db 1561 YVASAGKVRNKLKIQCLEGIMEQSCIPVCEPPPVPEGMYECTNFSLDSQCVL 1620
Qy 1621 NCNERREKLPLCTKBEGLMTOEFLCENLQCECPPPSSELSVYKCEQYGIGAVCSPL 1680
Db 1621 NCNERREKLPLCTKBEGLMTOEFLCENLQCECPPPSSELSVYKCEQYGIGAVCSPL 1680
Qy 1681 CVIPSPDPMVLENITADTLEHMMEPVKQSI VCTGRRQMPDVLVHCIOSECFQADG 1740
Db 1681 CVIPSPDPMVLENITADTLEHMMEPVKQSI VCTGRRQMPDVLVHCIOSECFQADG 1740
Qy 1741 WCDTINNRAYCHYDGDCCSSTLSSKKVIPPADCDLDECTCRDPAKENQ 1791
Db 1741 WCDTINNRAYCHYDGDCCSSTLSSKKVIPPADCDLDECTCRDPAKENQ 1791

```

RESULT 3
US-10-675-685-3
; Sequence 3, Application US/10675685
; Publication No. US20040063134A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: PB0114
CURRENT APPLICATION NUMBER: US/10/675, 685
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aecmca Sequence Listing Engine
SEQ ID NO 3
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
US-10-675-685-3

Query Match 99.8%; Score 9836; DB 15; Length 1791;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1788; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 MMCKILIRISLIALAGMALCSANSELGWTTRKSLVEREHLNOVLLEGRCHLGAQRPR 60
DB 1 MMCKILIRISLIALAGMALCSANSELGWTTRKSLVEREHLNOVLLEGRCHLGAQRPR 60
QY 61 ASPQHLFGVPSRAGNYLRPYVGEQEIHTGSRKPTEGNAVSLVPPDLTENPAGRG 120
DB 61 ASPQHLFGVPSRAGNYLRPYVGEQEIHTGSRKPTEGNAVSLVPPDLTENPAGRG 120
QY 121 AVEBPAAWVDSPIQSEELLGDDAYLGNORSKESLGEAGIÖKGSAMAATTTTAIFTL 180
DB 121 AVEBPAAWVDSPIQSEELLGDDAYLGNORSKESLGEAGIÖKGSAMAATTTTAIFTL 180
QY 121 AVEBPAAWVDSPIQSEELLGDDAYLGNORSKESLGEAGIÖKGSAMAATTTTAIFTL 180
DB 121 AVEBPAAWVDSPIQSEELLGDDAYLGNORSKESLGEAGIÖKGSAMAATTTTAIFTL 180
QY 181 NEPPETORGMWASRÖRÖYWKRAEDQGDSCGISHFÖPMPKSLKHYKKSPPRESN 240
DB 181 NEPPETORGMWASRÖRÖYWKRAEDQGDSCGISHFÖPMPKSLKHYKKSPPRESN 240
QY 241 ÖNGGGSYREAEFTNSÖVGLPILVFSSGRERLLLRPEYLARIPREAFTVEAMVREGÖN 300
DB 241 ÖNGGGSYREAEFTNSÖVGLPILVFSSGRERLLLRPEYLARIPREAFTVEAMVREGÖN 300
QY 301 NPALIAGVFDCNSHTVSDKGWALGIRSGDKDKDARFFSLCTDRVKKATILISHSYÖ 360
DB 301 NPALIAGVFDCNSHTVSDKGWALGIRSGDKDKDARFFSLCTDRVKKATILISHSYÖ 360
QY 361 PGITHTAATYDGRHMLYVDGTÖVASLDSGPIANSFPMASSCSLLIGDSSSDGHYR 420
DB 361 PGITHTAATYDGRHMLYVDGTÖVASLDSGPIANSFPMASSCSLLIGDSSSDGHYR 420
QY 421 GHLGTIVWSTALPOSHRÖHSSÖHSSGEEBATDVLTSFEPVNTWMPFRDEKYPREY 480
DB 421 GHLGTIVWSTALPOSHRÖHSSÖHSSGEEBATDVLTSFEPVNTWMPFRDEKYPREY 480
QY 481 LÖGFEPEPEILSPÖPLCGÖTVCDNVELISÖYNGWPLRGEKVIYÖVNNI CDBEGINP 540
DB 481 LÖGFEPEPEILSPÖPLCGÖTVCDNVELISÖYNGWPLRGEKVIYÖVNNI CDBEGINP 540
QY 541 IVSEEOIRLÖHEALNEAFSRYNISWÖLSVHÖVANSSTLRHVLYLVNCEPSKITGNDHCPEC 600
DB 541 IVSEEOIRLÖHEALNEAFSRYNISWÖLSVHÖVANSSTLRHVLYLVNCEPSKITGNDHCPEC 600
QY 601 EHPILGVGDGDCRLÖGRCYSMNRBDGLCHVECNMMLNDFDGDCCDPÖVAVRYKTCEDP 660
DB 601 EHPILGVGDGDCRLÖGRCYSMNRBDGLCHVECNMMLNDFDGDCCDPÖVAVRYKTCEDP 660
QY 661 SPKRAYSVKELKELÖQNSTHPLNTIYFASSVREDLAGAATWPMDKAVTHLGGLVLSPA 720
DB 661 SPKRAYSVKELKELÖQNSTHPLNTIYFASSVREDLAGAATWPMDKAVTHLGGLVLSPA 720
QY 721 YYGMPGHTDTMIHEVGHVGLIYHVPKGVSERES CNDPCKETVPSMETGDL CADA TP PPKS 780
DB 721 YYGMPGHTDTMIHEVGHVGLIYHVPKGVSERES CNDPCKETVPSMETGDL CADA TP PPKS 780
QY 781 ELCEPEPTSTÖGCTFPPGAPFNINMSYTDNCTDNFTPOVARMCYLDLVYÖQMTES 840
DB 781 ELCEPEPTSTÖGCTFPPGAPFNINMSYTDNCTDNFTPOVARMCYLDLVYÖQMTES 840
QY 841 RKPTPIPIPWVIGÖTKNSLTIHMLPRISGVVYRASGSLCGACTEDGTFRÖVYHTASSR 900
DB 841 RKPTPIPIPWVIGÖTKNSLTIHMLPRISGVVYRASGSLCGACTEDGTFRÖVYHTASSR 900
QY 901 RVCSSSGWTPPEEAVGPDDVÖPCEPSIÖAMSPEVHLIYHMMTVPCTEGCSLELFOHP 960
DB 901 RVCSSSGWTPPEEAVGPDDVÖPCEPSIÖAMSPEVHLIYHMMTVPCTEGCSLELFOHP 960
QY 961 VÖADTLTLMTWSFMESSÖVLFDEIILLENKESVHLGDLDFCCIPLTIKHLVHGKVSÖV 1020
DB 961 VÖADTLTLMTWSFMESSÖVLFDEIILLENKESVHLGDLDFCCIPLTIKHLVHGKVSÖV 1020
QY 1021 KVYTFDERIEIDALLTSÖPHSPLCSGCRPVRYÖVLDPFPASGLPVVVTSHHKKFTDVE 1080

DB 1021 KVYTFDERIEIDALLTSÖPHSPLCSGCRPVRYÖVLDPFPASGLPVVVTSHHKKFTDVE 1080
QY 1081 VTPGÖMYÖYÖVLARAGELGASPLNHIHGAIPVCGGKVSERLGEBCDDDLVSGGCS 1140
DB 1081 VTPGÖMYÖYÖVLARAGELGASPLNHIHGAIPVCGGKVSERLGEBCDDDLVSGGCS 1140
QY 1141 KVCELEBGFNCVGEPSLCYMEBGDGLCEPERKTSIYDCGITYPKYLDÖWATRAYSHE 1200
DB 1141 KVCELEBGFNCVGEPSLCYMEBGDGLCEPERKTSIYDCGITYPKYLDÖWATRAYSHE 1200
QY 1201 DKKKCPVSLVTGEBSHICTSYHBDLPNHRPLTGMPFCVASENETÖDRSÖPEBSLKE 1260
DB 1201 DKKKCPVSLVTGEBSHICTSYHBDLPNHRPLTGMPFCVASENETÖDRSÖPEBSLKE 1260
QY 1261 DEWVLKVCFNRRPGARAFI FLTTDGLVPGEHOQPTVLVLTÖVRSNHSIGTGSLCOH 1320
DB 1261 DEWVLKVCFNRRPGARAFI FLTTDGLVPGEHOQPTVLVLTÖVRSNHSIGTGSLCOH 1320
QY 1321 NPILINVTHTÖNVL FHTTTSVLNFSPPRVGISAVALRTSSRIGLSAPSNCSISEGÖNH 1380
DB 1321 NPILINVTHTÖNVL FHTTTSVLNFSPPRVGISAVALRTSSRIGLSAPSNCSISEGÖNH 1380
QY 1381 ÖGÖSCIRPCGKÖDSCPSLLLDHADVNVCTSIGGLMKCAITCÖRGFALÖASSGÖYIRPM 1440
DB 1381 ÖGÖSCIRPCGKÖDSCPSLLLDHADVNVCTSIGGLMKCAITCÖRGFALÖASSGÖYIRPM 1440
QY 1441 ÖKETILLTSSGHWÖNÖVSCIPVDCGVDPBLVYANANSCSEGTFLRCSISCVPPAKÖ 1500
DB 1441 ÖKETILLTSSGHWÖNÖVSCIPVDCGVDPBLVYANANSCSEGTFLRCSISCVPPAKÖ 1500
QY 1501 GLSPWLCTLEDGLMSLEPEVCKLECDAPITILANLLPHCLÖDNHDVGTICKYCKRGY 1560
DB 1501 GLSPWLCTLEDGLMSLEPEVCKLECDAPITILANLLPHCLÖDNHDVGTICKYCKRGY 1560
QY 1561 YVASAEGVRYNKLKTIÖCLEGGIWEÖGSCIPVCEBPFPVFEAGMYECTNGFSIDSCVL 1620
DB 1561 YVASAEGVRYNKLKTIÖCLEGGIWEÖGSCIPVCEBPFPVFEAGMYECTNGFSIDSCVL 1620
QY 1621 NCGÖERKELI LCTKESLWÖEFLCENLÖGECPPPELSNVEYKCEÖGIGAVCSPL 1680
DB 1621 NCGÖERKELI LCTKESLWÖEFLCENLÖGECPPPELSNVEYKCEÖGIGAVCSPL 1680
QY 1681 CVIPSPDWMLPENITADTLEHMMEPYKVSÖICTGRÖNHBPVLVHCLÖSCPEFOANG 1740
DB 1681 CVIPSPDWMLPENITADTLEHMMEPYKVSÖICTGRÖNHBPVLVHCLÖSCPEFOANG 1740
QY 1741 WCDTINNRAYCHYDGGDCSSTLSSKKVIPFADCDLDECTCRDPKAEÖNÖ 1791
DB 1741 WCDTINNRAYCHYDGGDCSSTLSSKKVIPFADCDLDECTCRDPKAEÖNÖ 1791

RESULT 4
US-09-983-10
Sequence 10, Application US/09827998
Patent No. US20020102252A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MDHÖRF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aecmicsa Sequence Listing Engine
SEQ ID NO 10
LENGTH: 1770
TYPE: PRT
ORGANISM: Homo sapiens

US-09-827-998-10

Query Match 96.5%; Score 9507; DB 9; Length 1770;
 Best Local Similarity 99.9%; Pred. No. 0;
 Matches 1732; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 MMCKIRISLIALAGNALCSANSELGTRKSLVEREHLNQVLLEGERCWLAKVRPR 60
 DB 1 MMCKIRISLIALAGNALCSANSELGTRKSLVEREHLNQVLLEGERCWLAKVRPR 60
 QY 61 ASPQHLFGVYPSRAGNYLRPYVGEQIHTTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120
 DB 61 ASPQHLFGVYPSRAGNYLRPYVGEQIHTTGRSKPDTEGNAVSLVPPDLTENPAGLRG 120
 QY 121 AVEBPAPWVGDSPIQSGELIGDDAYLGNORSKESJGAGIQGSAAMAATTTAIFPTL 180
 DB 121 AVEBPAPWVGDSPIQSGELIGDDAYLGNORSKESJGAGIQGSAAMAATTTAIFPTL 180
 QY 181 NEPEPTEORRGMASSRORQVKKRAEDQDGSIGSHFOPWPKHSLKHRYKSPREBN 240
 DB 181 NEPEPTEORRGMASSRORQVKKRAEDQDGSIGSHFOPWPKHSLKHRYKSPREBN 240
 QY 241 QNGEGSYREAEFTNSQVGLPILYSGRRERLLRPEVLAIPREAFTEAMVPRGQGN 300
 DB 241 QNGEGSYREAEFTNSQVGLPILYSGRRERLLRPEVLAIPREAFTEAMVPRGQGN 300
 QY 301 NPALIAVFNDCSTHVDKGMALGIRSGKDKGKADARFFSLCTDRYKATILISHRYQ 360
 DB 301 NPALIAVFNDCSTHVDKGMALGIRSGKDKGKADARFFSLCTDRYKATILISHRYQ 360
 QY 361 PGWTHAAATYDGHMMLYVDGTQVASSLDQSGPLNSPMASSCSLLGGSSSDGHYR 420
 DB 361 PGWTHAAATYDGHMMLYVDGTQVASSLDQSGPLNSPMASSCSLLGGSSSDGHYR 420
 QY 421 GHLGTLVFWSTALPOSHFOHSSQSSGEBEATDLVLTASFEPTVTEWPFDEKXPRLV 480
 DB 421 GHLGTLVFWSTALPOSHFOHSSQSSGEBEATDLVLTASFEPTVTEWPFDEKXPRLV 480
 QY 481 LOGEPEPELISPLQPLCGQTCVNDVLLISQYNGYPLRGEKVIYQVANI CDDEGLNP 540
 DB 481 LOGEPEPELISPLQPLCGQTCVNDVLLISQYNGYPLRGEKVIYQVANI CDDEGLNP 540
 QY 541 IVSEBQRILOHEALNEAFSRYNISWOLSYOVNHSSTRHRVVLVNCBPSKGNHCPREC 600
 DB 541 IVSEBQRILOHEALNEAFSRYNISWOLSYOVNHSSTRHRVVLVNCBPSKGNHCPREC 600
 QY 601 EHPITGVDGDCRLQGRCYSWNRDGLCHVECNMMLNDFDGDCCDQVADVKTCTFPD 660
 DB 601 EHPITGVDGDCRLQGRCYSWNRDGLCHVECNMMLNDFDGDCCDQVADVKTCTFPD 660
 QY 661 SPKRAYSVKELKALQLNSTHFLNIYFASVREBDLAGAATWPKDQAVTHLGGIVLSPA 720
 DB 661 SPKRAYSVKELKALQLNSTHFLNIYFASVREBDLAGAATWPKDQAVTHLGGIVLSPA 720
 QY 721 YGMBPGHTDMIHVGHVGLYHFKVSRERESCNDCKEIVBEMEGDLCADAPAPPKS 780
 DB 721 YGMBPGHTDMIHVGHVGLYHFKVSRERESCNDCKEIVBEMEGDLCADAPAPPKS 780
 QY 781 ELCREPEPTSDTCGTFRPGAFPTNMSYTDNCTDFTPNQVARMHCYLDLVYQMTES 840
 DB 781 ELCREPEPTSDTCGTFRPGAFPTNMSYTDNCTDFTPNQVARMHCYLDLVYQMTES 840
 QY 841 RKPLPIIPMVIGQTKSLTIHMLPISGVVYDRASGSLCACTEDGTFRQYVHTASSR 900
 DB 841 RKPLPIIPMVIGQTKSLTIHMLPISGVVYDRASGSLCACTEDGTFRQYVHTASSR 900
 QY 901 RVCDSSGYMTPEBAVGPVDVQCEPSLOAWSPEVHL YHNMNTVPCCTEGSLELLQHP 960
 DB 901 RVCDSSGYMTPEBAVGPVDVQCEPSLOAWSPEVHL YHNMNTVPCCTEGSLELLQHP 960
 QY 961 VOADTLTLMWTSFPMESSQVLFDEIILLENKESVHLGPLDTFCDIPLTIKLVHGKYSV 1020
 DB 961 VOADTLTLMWTSFPMESSQVLFDEIILLENKESVHLGPLDTFCDIPLTIKLVHGKYSV 1020

QY 1021 KVTTFDERIEIDALLTSQPHSLCSGCRPVRYOVLADPPASGLPVVYVTHSHKFTDVE 1080
 DB 1021 KVTTFDERIEIDALLTSQPHSLCSGCRPVRYOVLADPPASGLPVVYVTHSHKFTDVE 1080
 QY 1081 VTPGQMTQYVLABAGELGASPLNHIGHAPCGDGKYSERIGEECDODDLVSGDGS 1140
 DB 1081 VTPGQMTQYVLABAGELGASPLNHIGHAPCGDGKYSERIGEECDODDLVSGDGS 1140
 QY 1141 KVCELEBGFNCVGPBSLCYMYEGDICEPFEKRTSIVDCGIYTBKGYLDQMATRAYSHE 1200
 DB 1141 KVCELEBGFNCVGPBSLCYMYEGDICEPFEKRTSIVDCGIYTBKGYLDQMATRAYSHE 1200
 QY 1201 DKKCPVSLVTGEPHSLICTSYHBDLNNHRLTQWPFQVASENRTODDRSQPESGLKE 1260
 DB 1201 DKKCPVSLVTGEPHSLICTSYHBDLNNHRLTQWPFQVASENRTODDRSQPESGLKE 1260
 QY 1261 DEWMLKVCNRPGRARAFIFLTDDGLVPGHQPTVLYLTDVRSNHSIGTYGLSCQH 1320
 DB 1261 DEWMLKVCNRPGRARAFIFLTDDGLVPGHQPTVLYLTDVRSNHSIGTYGLSCQH 1320
 QY 1321 NPILINVTHTQNVLFHHTTSVLNFSPPRVGISAVALRTSSRIGLSAPSNCTISDEGQNH 1380
 DB 1321 NPILINVTHTQNVLFHHTTSVLNFSPPRVGISAVALRTSSRIGLSAPSNCTISDEGQNH 1380
 QY 1381 QGOSCTHPCGKODSCSLLDHDVYVNCSTISGGLMKCAITTCRGPALQASSGOYIRPM 1440
 DB 1381 QGOSCTHPCGKODSCSLLDHDVYVNCSTISGGLMKCAITTCRGPALQASSGOYIRPM 1440
 QY 1441 QKEILLTCSGSHMPOVNSCLPVDGVPDPSLVNANFSCSEGTFLKRSISCPYPAKQ 1500
 DB 1441 QKEILLTCSGSHMPOVNSCLPVDGVPDPSLVNANFSCSEGTFLKRSISCPYPAKQ 1500
 QY 1501 GLSPWLTCLEBDGLMSLEBYCKLECDAPILIANLPLPHCLQDNHDVGI CKYCKRGY 1560
 DB 1501 GLSPWLTCLEBDGLMSLEBYCKLECDAPILIANLPLPHCLQDNHDVGI CKYCKRGY 1560
 QY 1561 YVASASAGKVRNKLKIQCLEGGIWEQSGCTPVCEPPPVPEGMVCTGNSFSDQCVL 1620
 DB 1561 YVASASAGKVRNKLKIQCLEGGIWEQSGCTPVCEPPPVPEGMVCTGNSFSDQCVL 1620
 QY 1621 NCNEREKPLICTKBEGLMTOEFLCENLOGECPPEPSSELSVYKCEQIGIGAVCSPL 1680
 DB 1621 NCNEREKPLICTKBEGLMTOEFLCENLOGECPPEPSSELSVYKCEQIGIGAVCSPL 1680
 QY 1681 CVIPSPDPMVLPENITADTLEHMMEPVKVOSIVCTGRQWHPDVLVHCIOQCE 1734
 DB 1681 CVIPSPDPMVLPENITADTLEHMMEPVKVOSIVCTGRQWHPDVLVHCIOQCE 1734

RESULT 5
 US-10-675-685-10
 ; Sequence 10. Application US/10675685
 ; Publication No. US20040063134A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Shannon, Mark
 ; APPLICANT: Gu, Yizhong
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: PB0114
 ; CURRENT APPLICATION NUMBER: US/10/675,685
 ; PRIOR FILING DATE: 2003-09-30
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Aeonica Sequence Listing Engine
 ; SEQ ID NO 10
 ; LENGTH: 1770
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-675-685-10

Query Match 96.5%; Score 9507; DB 15; Length 1770;
 Best Local Similarity 99.9%; Pred. No. 0; Mismatches 2; Indels 0; Gaps 0;
 Matches 1732; Conservative 0;

1 MMCLIRISLIALAGMALCSANSELGWTNRKSLVEREHLNOVLLEGERCMGAKVRPR 60
 1 MMCLIRISLIALAGMALCSANSELGWTNRKSLVEREHLNOVLLEGERCMGAKVRPR 60
 61 ASPQHLFGVYPSASAGVLRPYRVEOEIHHTGRSKPDTEGNAVSLVPRDLTEMPAGIRG 120
 61 ASPQHLFGVYPSASAGVLRPYRVEOEIHHTGRSKPDTEGNAVSLVPRDLTEMPAGIRG 120
 121 AVEBPAPWVGDSPIQSELLGDDAYLGNORSEKSEAGSIQKGSAMATTTTATFTTL 180
 121 AVEBPAPWVGDSPIQSELLGDDAYLGNORSEKSEAGSIQKGSAMATTTTATFTTL 180
 121 AVEBPAPWVGDSPIQSELLGDDAYLGNORSEKSEAGSIQKGSAMATTTTATFTTL 180
 181 NEPRPETQRGMWAKSRQRQVWKRAEDQDGSISHPQWPRHSLKHYKKSPPRESN 240
 181 NEPRPETQRGMWAKSRQRQVWKRAEDQDGSISHPQWPRHSLKHYKKSPPRESN 240
 241 QNGEGSYREAFETNSQVGLPIFYSGRERLLRPEVLAIPREAFTEAMVPRREGON 300
 241 QNGEGSYREAFETNSQVGLPIFYSGRERLLRPEVLAIPREAFTEAMVPRREGON 300
 301 NPATIAGVFDCSHTVSDKGWALGIRSGKDKGRDARFFSLCTDRYKATILISHRYQ 360
 301 NPATIAGVFDCSHTVSDKGWALGIRSGKDKGRDARFFSLCTDRYKATILISHRYQ 360
 301 NPATIAGVFDCSHTVSDKGWALGIRSGKDKGRDARFFSLCTDRYKATILISHRYQ 360
 361 PGTWTHAATYDGRHMLLYDGTQVASSLDQSGPLNSPFMASCSLLLGDSSEHGXYFR 420
 361 PGTWTHAATYDGRHMLLYDGTQVASSLDQSGPLNSPFMASCSLLLGDSSEHGXYFR 420
 421 GHGLTVLWSTALQSHFQSHSSGHEEATDVLTAASFEPVTEWPFDEKXPRLV 480
 421 GHGLTVLWSTALQSHFQSHSSGHEEATDVLTAASFEPVTEWPFDEKXPRLV 480
 481 LGPEPEPEILSPQPLCGQTVCDNVELISQYNGYMPLEGEKTYRQVNNI CDEGLNP 540
 481 LGPEPEPEILSPQPLCGQTVCDNVELISQYNGYMPLEGEKTYRQVNNI CDEGLNP 540
 541 IVESEQIRLOHEALNEAFSRNISMQLSVHQNSTLRHVVLVNCEPSKIGNDHCEPC 600
 541 IVESEQIRLOHEALNEAFSRNISMQLSVHQNSTLRHVVLVNCEPSKIGNDHCEPC 600
 601 EHPITVGDGDCRQGRCSYWRNRDGLCHVECNMMLNDFDGDCCDPQAVNRKTCEDPD 660
 601 EHPITVGDGDCRQGRCSYWRNRDGLCHVECNMMLNDFDGDCCDPQAVNRKTCEDPD 660
 661 SPKRAYSVKELKALQNSTHPLNIYFASVREDLAGAATWMDKAVTHLGGIVLSPA 720
 661 SPKRAYSVKELKALQNSTHPLNIYFASVREDLAGAATWMDKAVTHLGGIVLSPA 720
 721 YGMPGHTDTHIEVGHVGLYHVEFKGVSERESNCPCKETVPSMETGDLCACTAPFPKS 780
 721 YGMPGHTDTHIEVGHVGLYHVEFKGVSERESNCPCKETVPSMETGDLCACTAPFPKS 780
 781 ELCEPEPTSTCGFTPRPGAPFTNYSYTDNCTDNTPNOVARMHCYLDLVYQOWTES 840
 781 ELCEPEPTSTCGFTPRPGAPFTNYSYTDNCTDNTPNOVARMHCYLDLVYQOWTES 840
 841 RKPPPIPLPVAIGQTNKSLFTIHLPRISGVVYRASGSLGCACTEDGTFRQYHTASSR 900
 841 RKPPPIPLPVAIGQTNKSLFTIHLPRISGVVYRASGSLGCACTEDGTFRQYHTASSR 900
 901 RVCDSSGVTPEEAIVGPEDVQCEPSLOAMSPEVHLVHMMNTVPCPTGSGSLLEFQHP 960
 901 RVCDSSGVTPEEAIVGPEDVQCEPSLOAMSPEVHLVHMMNTVPCPTGSGSLLEFQHP 960
 961 VQADTLTLMWTSFMESSQVLFDTBILLENKESVHLGLDFDCIPLTIKHLVHGKXSGV 1020
 961 VQADTLTLMWTSFMESSQVLFDTBILLENKESVHLGLDFDCIPLTIKHLVHGKXSGV 1020
 1021 KVVYFDRIRIIDAALLTSQPHSPICSGCRPVRYQVLRBPAPASGLPVVTVTHSHKFTDVE 1080

1021 KVVYFDRIRIIDAALLTSQPHSPICSGCRPVRYQVLRBPAPASGLPVVTVTHSHKFTDVE 1080
 1081 VTGQWYQYOVLAAGCELGASBPPLNHIGAPYCGGKXSERLGECCDDGLVSGGCS 1140
 1081 VTGQWYQYOVLAAGCELGASBPPLNHIGAPYCGGKXSERLGECCDDGLVSGGCS 1140
 1141 KVCELEBGFNCVGPSPCYMEGDIICEPERKTSIVDCGIYTPKGLDOMATRAYSHE 1200
 1141 KVCELEBGFNCVGPSPCYMEGDIICEPERKTSIVDCGIYTPKGLDOMATRAYSHE 1200
 1201 DKKCPVSLVTGEPHSLICTSYHDLPHNRPLTGMFPCVASENETODRSQEPGSLKKE 1260
 1201 DKKCPVSLVTGEPHSLICTSYHDLPHNRPLTGMFPCVASENETODRSQEPGSLKKE 1260
 1261 DEWMLKCFNRPEARAFIFLTTDGLVPEHQOPTYTLVLTDRGNSHSLGTGLSCOH 1320
 1261 DEWMLKCFNRPEARAFIFLTTDGLVPEHQOPTYTLVLTDRGNSHSLGTGLSCOH 1320
 1321 NPATIAVTHHQNVLPHHTTSVLTNPFSSPRVGSALVALRTSSRLGLSAPNSCISEDEQNH 1380
 1321 NPATIAVTHHQNVLPHHTTSVLTNPFSSPRVGSALVALRTSSRLGLSAPNSCISEDEQNH 1380
 1381 QGOSCHIRPCGKODSCSLLDHADVNCISIGBLMKCAITCQRFALQASSGOYIRPM 1440
 1381 QGOSCHIRPCGKODSCSLLDHADVNCISIGBLMKCAITCQRFALQASSGOYIRPM 1440
 1441 QKEITLTCSSGHDONVSCIPVDCGVDPBSLVNANANSCSEGRKFLKRCGISCVPRKQ 1500
 1441 QKEITLTCSSGHDONVSCIPVDCGVDPBSLVNANANSCSEGRKFLKRCGISCVPRKQ 1500
 1501 GLSPWLTCLEBDGLMSLPEVYCKLECDAPRIILNANLLPCLQDNHVGITCKYCKRPGY 1560
 1501 GLSPWLTCLEBDGLMSLPEVYCKLECDAPRIILNANLLPCLQDNHVGITCKYCKRPGY 1560
 1561 YVASEAGKVRNKLKIQCLEGGIWEQSCIPVCEPPPVFEEMVCTNGFSLDSQCVL 1620
 1561 YVASEAGKVRNKLKIQCLEGGIWEQSCIPVCEPPPVFEEMVCTNGFSLDSQCVL 1620
 1621 NCNOREKRLPLCTKEGLMTQEFKLCENLQGECPPEPSELNSVYKCEOGYIGAVCSPL 1680
 1621 NCNOREKRLPLCTKEGLMTQEFKLCENLQGECPPEPSELNSVYKCEOGYIGAVCSPL 1680
 1681 CVIPSPDPAWLPENITADTLEHMMEPVKVQSIYCTGRQWHPVLVHCIOQCE 1734
 1681 CVIPSPDPAWLPENITADTLEHMMEPVKVQSIYCTGRQWHPVLVHCIOQCE 1734

RESULT 6
 US-09-827-998-16
 ; Sequence 16, Application US/09827998
 ; Patent No. US20020102252A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gu, Yizhong
 ; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: mdmorf-8
 ; CURRENT APPLICATION NUMBER: US/09/827,998
 ; PRIOR FILING DATE: 2001-04-06
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Aeomica Sequence Listing Engine
 ; SEQ ID NO 16
 ; LENGTH: 1385
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-09-827-998-16

Query Match 74.7%; Score 7363; DB 9; Length 1385;
 Best Local Similarity 77.0%; Pred. No. 0;

Matches 1379;	Conservative 0;	Mismatches 6;	Indels 406;	Gaps 1;
Qy	1	MMCKLIRISLAIAGALCSANSELGWTKKSLVEEHLNOVLLEBERCMLAKXVRRPR	60	
Db	1	MMCKLIRISLAIAGALCSANSELGWTKKSLVEEHLNOVLLEBERCMLAKXVRRPR	60	
Qy	61	ASPOHHLFGVYPSRAGNYLPRYPVGEBOIHHTGSKSDTEGNAVSLVPPDLTENPAGLRG	120	
Db	61	ASPOHHLFGVYPSRAGNYLPRYPVGEBOIHHTGSKSDTEGNAVSLVPPDLTENPAGLRG	120	
Qy	121	AVEBPAPWVGDSPIGSELLGDDAYLGNQSKESLGEAGIQGSAAMAATTITLFTTL	180	
Db	121	AVEBPAPWVGDSPIGSELLGDDAYLGNQSKESLGEAGIQGSAAMAATTITLFTTL	180	
Qy	181	NEBPPELQRRGMKASRRQRYWKRRADGGDSGISSHFQWPFGSLKHYKYSPPRESN	240	
Db	181	NEBPPELQRRGMKASRRQRYWKRRADGGDSGISSHFQWPFGSLKHYKYSPPRESN	240	
Qy	241	ONGEGSYREAFETNSQVGLPIVFGSRREBLRLRPVLAIEIPREAFTEAMVWKEGON	300	
Db	241	ONGEGSYREAFETNSQVGLPIVFGSRREBLRLRPVLAIEIPREAFTEAMVWKEGON	300	
Qy	301	NPAIAGVFNCSHTTVSDKGMALGIRSGKDKGRADAFPSLCTDRYKAKATILISHSRQ	360	
Db	301	NPAIAGVFNCSHTTVSDKGMALGIRSGKDKGRADAFPSLCTDRYKAKATILISHSRQ	360	
Qy	361	PGTWHTVAATYDGRHMLYVDGTQVASSLDQSGPLNSPFMAKCSLLLGDSSEGHYFR	420	
Db	361	PGTWHTVAATYDGRHMLYVDGTQVASSLDQSGPLNSPFMAKCSLLLGDSSEGHYFR	420	
Qy	421	GHGLTVFWSTALPQSHFQHSQHSGBEATDVLTAEPVNTWVPRDEKYPRLV	480	
Db	421	GHGLTVFWSTALPQSHFQHSQHSGBEATDVLTAEPVNTWVPRDEKYPRLV	480	
Qy	481	LQGFEPPEILPLQPLCGQTVCDNVELISQYNGYPLRGEKVIYQVNNICDEGLNP	540	
Db	481	LQGFEPPEILPLQPLCGQTVCDNVELISQYNGYPLRGEKVIYQVNNICDEGLNP	540	
Qy	541	IYSEBOIRLOHEALNEAFSRYNISWOLSVHVNSTLRHRVVLNCEPSKIGNDHCDPEC	600	
Db	541	IYSEBOIRLOHEALNEAFSRYNISWOLSVHVNSTLRHRVVLNCEPSKIGNDHCDPEC	600	
Qy	601	EHLVTGVDGDCRLQGRCSYMNRRDGLCHYBCNNMLNPDGDCDQVADVRKTCRDP	660	
Db	601	EHLVTGVDGDCRLQGRCSYMNRRDGLCHYBCNNMLNPDGDCDQVADVRKTCRDP	660	
Qy	661	SPKRAVSVKELKALQLNSTHFLNIYFASVREDLAATAWPKDAVTHGLGIVLSPA	720	
Db	661	SPKRAVSVKELKALQLNSTHFLNIYFASVREDLAATAWPKDAVTHGLGIVLSPA	720	
Qy	721	YGMPEGHTDTMIEHGVHGLYHVFKGVSERESCNDECKETVPBMEGDLCAADTAPTPKS	780	
Db	721	YGMPEGHTDTMIEHGVHGLYHVFKGVSERESCNDECKETVPBMEGDLCAADTAPTPKS	780	
Qy	781	ELCREPPTSDTCGFRFPAGAPFTNWSYTDNCTDNFTNOVARMHCYLDLYVQQTES	840	
Db	781	ELCREPPTSDTCGFRFPAGAPFTNWSYTDNCTDNFTNOVARMHCYLDLYVQQTES	840	
Qy	841	RKCTPIPIPMVIGQTKSLTIHMLPISGVVYDRAGSLCAGATEBGTFRQVYHTASSR	900	
Db	841	RKCTPIPIPMVIGQTKSLTIHMLPISGVVYDRAGSLCAGATEBGTFRQVYHTASSR	900	
Qy	901	RVCDSGYWTPPEAVGPDPVQCEPSLQAWSPEVHLYHNMNTVPCTEGCSLELFLQHP	960	
Db	901	RVCDSGYWTPPEAVGPDPVQCEPSLQAWSPEVHLYHNMNTVPCTEGCSLELFLQHP	960	
Qy	961	VOADTLTLMWTSFPMESSQVLPDEILLENKESVHLGRLTFCDIPITIKLHVDGKVS	1020	
Db	961	VOADTLTLMWTSFPMESSQVLPDEILLENKESVHLGRLTFCDIPITIKLHVDGKVS	1020	
Qy	1021	KVYTFDERIRIDALLTSQPHSLCSCGRPVYQVLDPPASGLPVVYVTHSHRKFTDVE	1080	
Db	1021	KVYTFDERIRIDALLTSQPHSLCSCGRPVYQVLDPPASGLPVVYVTHSHRKFTDVE	1080	

Qy	1081	VTPGQWYQVOLAEGAGELGASPLNHIHGAIPYCGDKVSEBRLGECDDGDLVSGDGS	1140
Db	675	VTPGQWYQVOLAEGAGELGASPLNHIHGAIPYCGDKVSEBRLGECDDGDLVSGDGS	734
Qy	1141	KVCELEBGFNCVGBPSLCYMEYDGLCEPPEKRTSIVDCGIYYPKYLDOMATRAVSSHE	1200
Db	735	KVCELEBGFNCVGBPSLCYMEYDGLCEPPEKRTSIVDCGIYYPKYLDOMATRAVSSHE	794
Qy	1201	DKKCPVSLVTGBPHSLICTSYHBDLPNHRPLTGMFPCVASENETODDRSEQPEGLKKE	1260
Db	795	DKKCPVSLVTGBPHSLICTSYHBDLPNHRPLTGMFPCVASENETODDRSEQPEGLKKE	854
Qy	1261	DEWMLKCFNRPGEARAIFLFTTDLGVPEHQOPTYTLVLTVRGSNHSIGTGSLCQH	1320
Db	855	DEWMLKCFNRPGEARAIFLFTTDLGVPEHQOPTYTLVLTVRGSNHSIGTGSLCQH	914
Qy	1321	NPLIINTVHHQNVLFHHTTVLNLNFSPPRGISAVALRTSSRIGLSAPSNCSISEGQNH	1380
Db	915	NPLIINTVHHQNVLFHHTTVLNLNFSPPRGISAVALRTSSRIGLSAPSNCSISEGQNH	974
Qy	1381	QGGSCIHPCGKQDCSCLLDHADVVNCTSIGGLMKCAITTCQGFALQASSGQYIRPM	1440
Db	975	QGGSCIHPCGKQDCSCLLDHADVVNCTSIGGLMKCAITTCQGFALQASSGQYIRPM	1034
Qy	1441	QKEILLTCCSGHNDQVNSCLPVDGVPDPSLVNANFSCSEBGTFLRCSTICVPKALQ	1500
Db	1035	QKEILLTCCSGHNDQVNSCLPVDGVPDPSLVNANFSCSEBGTFLRCSTICVPKALQ	1094
Qy	1501	GLSPWLTCLEBDGLWSLPEVYCKLECDAPRIILNANLLPCLQDNHNVGTICKYECRPGY	1560
Db	1095	GLSPWLTCLEBDGLWSLPEVYCKLECDAPRIILNANLLPCLQDNHNVGTICKYECRPGY	1154
Qy	1561	YVASEAGKVRNKLKIQCLEGGIWEQSGCIPVCEBPPVPEBMEYCTNGFSLDSQCVL	1620
Db	1155	YVASEAGKVRNKLKIQCLEGGIWEQSGCIPVCEBPPVPEBMEYCTNGFSLDSQCVL	1214
Qy	1621	NCNOERKELPILCTKESLMQOEFKLCENLOGECPRPSELNVSVEYKKEQYIGAVCSPL	1680
Db	1215	NCNOERKELPILCTKESLMQOEFKLCENLOGECPRPSELNVSVEYKKEQYIGAVCSPL	1274
Qy	1681	CVLPSPDPVWLPEKITADTLEHNMPEPVKQSIYCTGRQNHPPDLVHVCISQCEPQADG	1740
Db	1275	CVLPSPDPVWLPEKITADTLEHNMPEPVKQSIYCTGRQNHPPDLVHVCISQCEPQADG	1334
Qy	1741	WCDTINNRAYCHYDGGDCSSTLSKKVIRPADCDLDECTCRDPKAEHQ	1791
Db	1335	WCDTINNRAYCHYDGGDCSSTLSKKVIRPADCDLDECTCRDPKAEHQ	1385

RESULT 7
 US-10-675-685-16
 ; Sequence 16, Application US/10675685
 ; Publication No. US20040063134A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Gu, Yizhong
 ; APPLICANT: Shannon, Mark
 ; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
 ; FILE REFERENCE: PB0114
 ; CURRENT APPLICATION NUMBER: US/10/675,685
 ; CURRENT FILING DATE: 2003-09-10
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 60/236,359
 ; PRIOR FILING DATE: 2000-09-27
 ; NUMBER OF SEQ ID NOS: 1881
 ; SOFTWARE: Acemica Sequence Listing Engine
 ; SEQ ID NO 16
 ; LENGTH: 1385
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 US-10-675-685-16

Query Match 74.7%; Score 7363; DB 15; Length 1385;
 Best Local Similarity 77.0%; Pred. No. 0;
 Matches 1379; Conservative 0; Mismatches 6; Indels 406; Gaps 1;

QY 1 MMCIKLIRISLAIAGALCSANSELGWTTRKSLIVEREHLNOVLLBEGRCMLGAKVRPR 60
 DB 1 MMCIKLIRISLAIAGALCSANSELGWTTRKSLIVEREHLNOVLLBEGRCMLGAKVRPR 60
 QY 61 ASPOHHLFGVYPASAGVYLPRYPVGEBOIHHHTGSKPDTEGNANSLVLPDLTENPAGLRG 120
 DB 61 ASPOHHLFGVYPASAGVYLPRYPVGEBOIHHHTGSKPDTEGNANSLVLPDLTENPAGLRG 120
 QY 121 AVEBPAPWVGDSFIQSGELGDDAYLGNQSKESLGEAGIQKSGMAAATTTTAIFTL 180
 DB 121 AVEBPAPWVGDSFIQSGELGDDAYLGNQSKESLGEAGIQKSGMAAATTTTAIFTL 180
 QY 181 NEPKETORRGMAKSRORROYWKRAEDQGDGSISSHFOQWPGHSLKHYKKSPPRESN 240
 DB 181 NEPKETORRGMAKSRORROYWKRAEDQGDGSISSHFOQWPGHSLKHYKKSPPRESN 240
 QY 241 ONGEGSYREAFETNSQVGLPILYFSGRRERLLRPEVLAIEPREAFTEAMVKEGON 300
 DB 241 ONGEGSYREAFETNSQVGLPILYFSGRRERLLRPEVLAIEPREAFTEAMVKEGON 300
 QY 301 NPAILAGVPDNCSTHTVSDKGWALGIRSGDKGRDAEFFSLCTDRVKAATILLISHRYQ 360
 DB 301 NPAILA----- 306
 QY 361 PGWTHVAATYDGRHMAALYVDGTQVASSLDQSGPLNPFMAKSCSLLLGDSSEGHYFR 420
 DB 307 ----- 306
 QY 421 GHGLTVFWSIALPQSHFQHSQSSGEBEATDLVLASFEPTVTEWVPRDEKYPRLV 480
 DB 307 ----- 306
 QY 481 LQGEPEPEILSLQPLPQGTQVCDNELLSQYNGWPLRGEKVIYQVNNICDEGLNP 540
 DB 307 ----- 306
 QY 541 IVSEBQIRLOHEALNEAFSRNYSWQLSVQVHNSLTHRVVLVNCESPKIGNDHCEPC 600
 DB 307 ----- 306
 QY 601 EHLPLGYDGDGCRLOGRCYSWNRBDGLCHVSCNNMLNDFDGDCCDPQVADVKTCTPDP 660
 DB 307 ----- 306
 QY 661 SPKRAVSVKELKEALQJNSTHPLNIYFASVREDLAATWPKDAVTHLGGIVLSPA 720
 DB 307 -----GGIVLSPA 314
 QY 721 YYGMPGHTDTHIEVGVHLGLYHFKGVSERESNDDPKETVPSMETGDLCAITAPTPKS 780
 DB 315 YYGMPGHTDTHIEVGVHLGLYHFKGVSERESNDDPKETVPSMETGDLCAITAPTPKS 780
 QY 781 ELGEEPRPTSGFTFPGAPFTNMYSTYDNCIDNFTPQVARMCIYDLVYQOMTES 840
 DB 375 ELGEEPRPTSGFTFPGAPFTNMYSTYDNCIDNFTPQVARMCIYDLVYQOMTES 840
 QY 841 RKPTPIPIPMVNIQOTNKSLLTIHMLPISGVYVDRASGLSCAGCTEDGTFRQVYHTASR 900
 DB 435 RKPTPIPIPMVNIQOTNKSLLTIHMLPISGVYVDRASGLSCAGCTEDGTFRQVYHTASR 900
 QY 901 RVCDSGWTPEEAIVGPPVDVQCEPSIQAMSPEVHLVHMNTVPCPTGEGSLBLRQHP 960
 DB 495 RVCDSGWTPEEAIVGPPVDVQCEPSIQAMSPEVHLVHMNTVPCPTGEGSLBLRQHP 960
 QY 961 VQADTLTLMTWSFMESSQVLFTEILLNESVHLGDLFFCQILPLTIKLVHVGKXSV 1020
 DB 555 VQADTLTLMTWSFMESSQVLFTEILLNESVHLGDLFFCQILPLTIKLVHVGKXSV 1020
 QY 1021 KVYTFDERIEIDALLTSQPHSLCSGCRPVRYQVLDPFPASGLPVVVTSHRKTDFVE 1080

DB 615 KVYTFDERIEIDALLTSQPHSLCSGCRPVRYQVLDPFPASGLPVVVTSHRKTDFVE 674
 QY 1081 VTBGQWYQYOVUVAEAGGEAGEASPRLNHIGARYCGDGKXSEBLGECDDGDLVSGDGS 1140
 DB 675 VTBGQWYQYOVUVAEAGGEAGEASPRLNHIGARYCGDGKXSEBLGECDDGDLVSGDGS 1140
 QY 1141 KVCELEBGFNCVGEPSLCYVMEGDGICEPERKTSIVDCGIYTPKGYLDQMATRAYSHE 1200
 DB 735 KVCELEBGFNCVGEPSLCYVMEGDGICEPERKTSIVDCGIYTPKGYLDQMATRAYSHE 1200
 QY 1201 DKXKCPVSLVTGPHSLICTSYHDPDLPNHRPLTGWPCVASEWETODDBEOPBGSILKE 1260
 DB 795 DKXKCPVSLVTGPHSLICTSYHDPDLPNHRPLTGWPCVASEWETODDBEOPBGSILKE 1260
 QY 1261 DEVMKVCENRPGEARAIFLFTTDLGVGEHOOPVTLVLTGVRGNSHSLGTGSLSCOH 1320
 DB 855 DEVMKVCENRPGEARAIFLFTTDLGVGEHOOPVTLVLTGVRGNSHSLGTGSLSCOH 1320
 QY 1321 NPLIINTVTHQNVLFHHTTSVLLNFSFPRVGSVAVALRTSSRIQLSAPNSCISEDECONH 1380
 DB 915 NPLIINTVTHQNVLFHHTTSVLLNFSFPRVGSVAVALRTSSRIQLSAPNSCISEDECONH 1380
 QY 1381 QGQSCIHPCGKODSCPSLLDHDADVNCISIGPGLMKCAITQORFALQASSGOYLRPM 1440
 DB 975 QGQSCIHPCGKODSCPSLLDHDADVNCISIGPGLMKCAITQORFALQASSGOYLRPM 1440
 QY 1441 QKRIILLTSSGHHNDQVNSCLPVDGVPDPSLVNANFSCSEGTKFLKRCISICVPAKLQ 1500
 DB 1035 QKRIILLTSSGHHNDQVNSCLPVDGVPDPSLVNANFSCSEGTKFLKRCISICVPAKLQ 1500
 QY 1501 GLSPWLTCLEDDGLMSLPEVYCKLECDAPRIILNANLLPHCLQDNHDVGTICKYCKRGY 1560
 DB 1095 GLSPWLTCLEDDGLMSLPEVYCKLECDAPRIILNANLLPHCLQDNHDVGTICKYCKRGY 1560
 QY 1561 YVABSAGKVRANKLKTQCEJEGIWEQSGCIPVCEPFPVFEGMTYCTMGFSLDSQCVL 1620
 DB 1155 YVABSAGKVRANKLKTQCEJEGIWEQSGCIPVCEPFPVFEGMTYCTMGFSLDSQCVL 1620
 QY 1621 NCMOEREKLPILCTKESLMTQEPFLCENLQGECPPEPSELSNVEYKCEQGYGIGAVCSPL 1680
 DB 1215 NCMOEREKLPILCTKESLMTQEPFLCENLQGECPPEPSELSNVEYKCEQGYGIGAVCSPL 1680
 QY 1681 CVIPSPDPVMLPENITADTLEHMMEPVKVQSIYCTGRQWHPVLVHCTIQSCFPQADG 1740
 DB 1275 CVIPSPDPVMLPENITADTLEHMMEPVKVQSIYCTGRQWHPVLVHCTIQSCFPQADG 1740
 QY 1741 WCDTINNRAVCHYDGDCCSSTLSSKKVIPPADCDLDECTCRDPKAEENQ 1791
 DB 1335 WCDTINNRAVCHYDGDCCSSTLSSKKVIPPADCDLDECTCRDPKAEENQ 1791

RESULT 8
 US-09-983-025-25
 : Sequence 25, Application US/09983025
 : Publication No. US20030124529A1
 : GENERAL INFORMATION:
 : APPLICANT: OXYVIG, Claus
 : APPLICANT: OVERGAARD, Michael T.
 : TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)
 : FILE REFERENCE: OXYVIG-1A
 : CURRENT APPLICATION NUMBER: US/09/983, 025
 : CURRENT FILING DATE: 2001-10-22
 : PRIOR APPLICATION NUMBER: US 60/241, 840
 : PRIOR FILING DATE: 2000-10-20
 : PRIOR FILING DATE: 2000-10-20
 : NUMBER OF SEQ ID NOS: 25
 : SOFTWARE: PatentIn version 3.1
 : SEQ ID NO 25
 : LENGTH: 1627
 : TYPE: PRT
 : ORGANISM: Homo sapiens


```
; PRIOR FILING DATE: 2001-12-14
; PRIOR APPLICATION NUMBER: US 60/347,211
; PRIOR FILING DATE: 2002-01-08
; PRIOR APPLICATION NUMBER: US 60/347,349
; PRIOR FILING DATE: 2002-01-10
; PRIOR APPLICATION NUMBER: US 60/355,250
; PRIOR FILING DATE: 2002-02-08
; PRIOR APPLICATION NUMBER: US 60/356,714
; PRIOR FILING DATE: 2002-02-13
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 1386
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO: 663
; LENGTH: 1627
; TYPE: PR1
; ORGANISM: Homo sapiens
US-10-295-027-663

Query Match      39.7%; Score 3916.5; DB 15; Length 1627;
Best Local Similarity 45.8%; Pred. No. 1.3e-289;
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

QY 249 REAATFNSQGLP--ILYFSGRRL--LAPETLAETPREAFVYBAWYKPGGQNNPAII 305
D 80 REARGATEEPPSPRALYFSGRGEQLRYLRADL--ELPRDAFTLQVMLRAEGGQSPAVI 137
QY 306 AGVDNCSHTVSDGMAIGRSGDKGKRDARFFPSLCTDRVKKATLISHRYQPGWT 365
D 138 TGLYDKCSYSRDRGMVGHHTISDQDKDPRYFSLKTDARAVTTINARSTYLPQMV 197
QY 366 HVAATYGRHMAALYVDGTQVNASLDSGPLNSPFMACRSLLGDSSEDDHYRGLGT 425
D 198 YLAATYGGQFKLYVNGAQVATSGEYQVGIISPLQCKVLMGG--SALNNHNRGIIEN 255
QY 426 LVFVSTALPQSHFOHSSQHSSEBEATDVLVTASFEPVTEWVPREDKYPRLEV--LQG 483
D 256 FSLMKVARTORELISDMETHGAHTALPOLQENMDVNVKHAMSPKQSSPKVAFVSNAG 315
QY 484 FEPRPILSPLOPLCGQTVCDNVETLSQVNGWYPLRGEKXIRQOVNICDDEGLNPIVS 543
D 316 FLUD---TSLRPPLCGQTLCDNTEVASTYQSSFPQPKVRRVNVLYEDDKNFTVT 371
QY 544 BEQIRLOHBALEAFSRYNISWQLSVHVNSTLRHRVVLVNCBPSKIGNDHCDPECEHP 603
D 372 REQYDFQHQAALAEAFKQYINISMELDVLVENSLSARRLLILANCOISKIGDNCPECNHT 431
QY 604 LTGYDGDGR--LQGRCTSNRRDGLCHVECNMLNDPDDGCCPQVADYAKTCFDPDSP 662
D 432 LTGHGDGDCRHLRPAFVKQKHNGVCDMDCYERFNFPGGECDPBEITNVYQTCFDPDSP 491
QY 663 KRAWSTYKELKEALQOLMSTHFLINYPASSVREDLAAGATWPMDDATVHIGIYLSPAY 722
D 492 HRAVLVDNELKNIKLKLGSTHLNIFPAKSSSEELAGVATWPMDEKALMHLGIVLNSPY 551
QY 723 GMPGHTDMIEHGVHVLGYHVFKGVSERESCNDRCKETVPSMETGLCADTAPPSSEL 782
D 552 GMPGHTDMIEHGHSLGYHVFGRGISEIOCSDPCKMETEFSFETGULCNDTNAPRHS 611
QY 783 CREDEPTSDTCGTPRPGARPNTMSTYDNCSTNFTPNQVARNHCVLIDVYQWTESRK 842
D 612 CGDPGPNADTCGFHSFNTPYNNFMSYADDCTDSTFTPNQVARNHCVLIDVYQWQMSRK 671
QY 843 PTPRIPRMVYIGQNKSLTIHMLRPIGUVVYDRASSGLCGACTPDGTFRRQVNHASSRV 902
D 672 PAVPALAPQVAGHTDVTLEMPPIIDGHFERELGASCHLCLEGRILVQANASSBMP 731
QY 903 CDSGGYTPREAVGPVVDQCEPSLQAMSEVLYLHNMNTVP--TEGSLIELLFOHPV 961
D 732 CSBPGHMSPREABEHPRVDEQCKSSVATKSNVSNVHNTVPACRPEQCGTLELEFLYPL 791
QY 962 QADTLILMTV--SFMSSSOVLPTTEILLENKESVHLGPDLPDIPVTKL--HVDKVS 1018
D 792 VPESLTIWTVFVSTDMDSGAVNDIKLAVAGKNISIGPQVFCVDFVLTIRLMVDEEVY 851
```

```
QY 1019 GVKVYTFDERIEIDAALLTSOPHSPLCSGCRPVRYQVLRDPPFASGLPVVYTHSRKFTD 1078
D 852 GIGYITLDEHLEIDAMLTSTADTPLCQCKPLKVKVRRPPLQMDVASTL--HNKRKFVD 910
QY 1079 VEYTPGMYQYVLAERAGSELGEASRPLNHIGAPYCGDGKVSERIGECCDDGLVSGDG 1138
D 911 MDNLGSGVYQVWYITISGTESESPSPAVYIHRGQYCGDGIIOKDQGECCDDMKIKINGD 970
QY 1139 CSKYCELEBGFNCVGEBSLCYMYEGDICEPFRKTSYVCCGYTPMGYLDONATRYSS 1198
D 971 CSLFRCQEVSNFICIDESPSCYFHDGDVCEFEQKTSIKCGGYTTPGGLPQDMASNSVS 1030
QY 1199 HEDKKCPVSLYTGEP--HSLICTSYHBDLPNHRPLTMGPFVASENTEQDRSEQPGESL 1257
D 1031 HOD--QCCPGWVITIGQPAASQVCKTKVIDLSEGISQAHMYCTTISYPSQ----- 1078
QY 1258 KKEDEVMLKVCFNRRPGEARAFIFLTTDGLVPGEHQPTVTLVYLDVRSNHSIGTYGLS 1317
D 1079 LAQTFMLRAYFSQPMVAALVIVHLVTDGYGQKQETISVOLDTKQDSHDLGLHYLS 1138
QY 1318 CQHNPLIINTYHQNVLFFHTTSVLNFSPPRGISAVALTSTSRIGLSAPNSCISDEG 1377
D 1139 CRNNPLIIPVHDLQEPFYHQAVRVSFSSPLVAISGVALRSDFNEDPVTLLSSC--QGET 1197
QY 1378 QNHQSGCIRPCGKODSCPSLLDDHADVNCSTI-----GPGIMKCAITGCRGALQASS 1433
D 1198 YSPRQSCVYFAEKTID--CEBLAVENAS--LNCSSDRYHG---AQCTVSCRTGYVLDIIR 1252
QY 1434 GQYIRPMQ--KEILITCSSGHMDONVSCLPVDCVDPDPSLVNANYANFSGSEGTFLKRCST 1491
D 1253 DDELISQGTSPVTVTCTEBGKMKQVACEPVDSCIPDHQVVAASFSCPGTFFGSCSF 1312
QY 1492 SCVPRAQLQSLSTWLTLEBGLMSLPREYCKLECDAPRILNANLLPHCLQDNHVGTI 1551
D 1313 QCRHPAQLKANNLLTCTMEDGLMSFPALCELMCLAPPVADNLOTARRENHKKVGSF 1372
QY 1552 CKYECKRGYVVAASAEKVNKLLKIQCLEGGIMEQSCIPVCEPPRPFEGMYECTNG 1611
D 1373 CKYKCRGHVNPSSR--KSKKRAFKQCTQDGSQWQBACACVPYCDPPRFHGLYQCTNG 1431
QY 1612 FSLDSQCVLNC-----NQEREKPLICTYEGMLTQEFKLCENLQGCBCPPPSSELS--VEY 1665
D 1432 FQFNSEGRICICEPDSADQGLGSNVHICRQKGTWNGSFHYVQEQMGQC--SVYNEINSLKL 1490
QY 1666 KCEQYIGAVSCPLCYIPSPDVMLEPNTATLTLEHMEPVVQSVYVCGRRQWHPDV 1725
D 1491 QCPDGYAIGSECATSCIDHNSESILIPMNVTVRDIIPHMLPTEVERVYCTAGLKMYPHA 1550
QY 1726 LVHICISCEPFOADGWCOTIINRAYCHYDGDCCSSTLSSKXYLPFAADCDLD--ECTCRD 1784
D 1551 LTHCVKCEPFPMDNYTCDAINNPAFCNYDGGDCTSTVTKKVTYPRFMSCDLQGDACARD 1610
QY 1785 PKAEN 1790
D 1611 PQAQEH 1616

RESULT 10
US-10-783-311-1
; Sequence 1, Application US/10783311
; Publication No. US2005009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAPP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
```

```

: SEQ ID NO 1
: LENGTH: 1627
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-783-311-1

Query Match      39.7%; Score 3916.5; DB 17; Length 1627;
Best Local Similarity 45.8%; Pred. No. 1.3e-289;
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

QY 249 REAETFSQVGLP--ILYFSGRRL--LRLPEVLAIEIPRAFTVEAWKPGGONPAII 305
DB 80 REARGATEBSPSRALYFSGRGEQLRLRADL--ELPRDAFTLQVWLRAEGGQSRPAVI 137
QY 306 AGVNDNSHYSDGMALGIRSGDKGRDARFPFSLCTDRAVKAATILISRRQPTWT 365
DB 138 TGLDCKSYISRDGMVVGHTISDODKDPFYFSLKTDRAQVTTINARSYLPQMV 197
QY 366 HVAATYDGRHALVVDGQVASSLDGSLPMAFCRSLLGDSSEGHYFRHLGT 425
DB 198 YLAFTYDQFMKLYVNGAQTSGVGGIFSLTQCKVLMG--SALNHNKRGYIEH 255
QY 426 LVFWSTALPQSHFQSSQSSGSEBETDVLVTASFEVNTVEVFERDEKYRLV--LQ 483
DB 256 FSLKLVARTQREILSDMETHGAHTALPQLLQEMNDVKAHMSPKVFEFSNAG 315
QY 484 FEPPELISLPQPLCGCTVCDNVELISQYNGYPLRGEKIRYQVNICDDEGLNPIVS 543
DB 316 FLID---TSLRPLCGQLCDNTEVLAAYQLSSFRQKVRVAVNLYEDHKNPVT 371
QY 544 EEOIRLOHEALNEAFSRYNISMOISYQVHNSTLRHVVLVLCSPSKIGNDHCPGCHP 603
DB 372 REQVDFQHHQLAERFKQINISWELDLVENSLSRRRLILANCOISKIDENCPGCHNT 431
QY 604 LTYGDGDCR--LQGRCYSWNRDGLCHVECNMNLNDPDDGCCDPOVADYAKTCFDDSP 662
DB 432 LTGHGDDCRLHRAFAFKQHGNCVCMDCYERFNFQSGCCDPEITNVQTCFDDSP 491
QY 663 KRAMSYKELKALQNLSTHFLNTYFASVREDLAGAATWWDYDVAATHLGGIYLSPAY 722
DB 492 HRAVLDNELKNILKLDGSTHLNIFAKSSEBELAGVATWPMDEALMHLGILNPSFY 551
QY 723 GMPGHTDTMHEVGVLYHVFKEGVBRESNDPCKETVPSMETGDLCDTAPTPSEL 782
DB 552 GMPGHTDTMHEIGHSLGLYHVFGRISBIOGSDPCHETEPSFTGDLCDNTNAPRKS 611
QY 783 CREBPTSDTCGFTFPGARPTNMYSTYDNCNTNFTPNQVARNMCHYLDLVYQOOTESRK 842
DB 612 CGDGPENDTCGFHSFNTFPNNMSTADDDCTSTFPNQVARNMCHYLDLVYQOOTESRK 671
QY 843 PTPIPDPVYIGQTNKSLTTHMLRPIGUVYDRAAGSLCAGCTEDGTFRQYVATSSRV 902
DB 672 PAPALAPQVYGHNTDVTLEMPPIQHFPERELGSCACHLGRILVQVYASNASBMP 731
QY 903 CDSGVTTPREAVPVDQRCERSLOAMPBVLHNMNTVPCP--TEGCELELFGHPV 961
DB 732 CSPGSHSPRAEHPVQPCSSVKTSSPNSAVNPHTPAPCPQGCYLELEFLYPL 791
QY 962 QADULTLMTV--SEPMESQVLPFTTEILLENKESVHLGPTDFCDIPTIKL--HYDGV 1018
DB 792 VPBSLTIWTFVSLDMDSSGAVNDIKLAVSGKNISLGPQVPCDVPDLTIRLMVDEEV 851
QY 1019 GVKVYTFDERIEIDALLTQSPHPLCSGCRPVRYQVLRDPPFASGLPVVVTSHRKPTD 1078
DB 852 GIQYITLDEHLEIDAMLTSTADTPLCLQCKPLKTKVVRDPLQMDVASIL--HNRRFVD 910
QY 1079 VEVTPGMQYQVLAAGELGEASPLNHTHGAHYCGDGVSRLESECDGDLVSDG 1138
DB 911 MDLVLGYQVQWVTTISGTESESPAVTYHGRGCGDGIQKQGGQCDMMKINGDG 970
QY 1139 CSKVCLEBEGFNACVGBPSLCTMYEGDGICEPFRKTSIVDCGIYTPKGYLDQWATRAY 1198
DB 971 CSLPCLREVSFNCIDEPSCVCFHDGDVCEFEQKTSIKDCGVYTTPGFLDQWASNSVS 1030

```

```

QY 1199 HEDKKCPVSLVNGEP--HSLICTSYHPLDPNHRPLTGMPCVASSENEDODRSRQPSGL 1257
DB 1031 HQD-QQCPGWIYIGQPARASQVCKTKVYIDLBSGISQHAMPTCTTISYPSQ----- 1078
QY 1258 KKEDEWMLKVCFNRCGEARAFIFLPTDGLVPGHQPTVLYLTDVRSNHSIGTYGLS 1317
DB 1079 LAQTFPLRAVFSQPMVAAYVIALYTDGYGQKQETISVQLDTRKDSHDLGLVLS 1138
QY 1318 QCNHPLIINTVHONVLFHHTSVLLNFPSSPRVIGSAVALRTSRIGLSAPNSCISEDEG 1377
DB 1139 CRNNPLIIPVHDLISQPFYHSQAVRVSFSSPLVAISGVALRSEFNPVLTSSC-ORGET 1197
QY 1378 QNHQGSCTHRPQCKOSCSLLLDHADVNCISI----GPKMKCAITQORGALQASS 1433
DB 1198 YSPAGSCVHPACKTD--CPFLAVENAS--LNCSSSDRYHG--AQCTVSCRTGYVLQIRR 1252
QY 1434 GQVTRPMQ--KEILTSCGHMDQNVSCLPVDCVPPPSLVNVAHFSCSEGTFLKRCST 1491
DB 1253 DDELIXQGTGSPSVYVCTEGKMKQVACEPVDGSIIPHQVYASFSCEPBTTFGSCSF 1312
QY 1492 SCVPPAKLQGLSPWLTLEDGLMSLPEVYCKLBEDAPPIILNALLPHCLQDNHVGTT 1551
DB 1313 QCRHPAQLKGNNSILTCMEDGLWSPFALCELMCLAPPVANDLQYARCRENHKYGVSF 1372
QY 1552 CKYCKRGYVYABAEKGVANKLKIQCLEGIMQSSCTPVNCEPPEPVPEGVECTNG 1611
DB 1373 CKYCKRGYVYABAEKGVANKLKIQCLEGIMQSSCTPVNCEPPEPVPEGVECTNG 1431
QY 1612 FSLDSQCVLNC-----NQEREKPLLTCKEGLMTOEKLCENLQGECPPEPSLNS--VEY 1665
DB 1432 FQFNSERICEDSDASQIGLSNVYHCRKQGTNNGSHVQCEMGQC--SVNELNSMUKL 1490
QY 1666 KCEQYIGAVCSPLCVIPSPDPVMLPENITADTLEHMEBVKVQSIYCTGRQWHPDV 1725
DB 1491 QCPGVAIGSEBACATSCIDHNSSEIILPMNTVARDIPMLNPTVERVYVCTAGLKMYRPA 1550
QY 1726 LVNHCISCEPQADGMCDDTINRAYCHYDGDCCSSSTLSKVIYPADCDL--ECGRD 1784
DB 1551 LHHVCKCEPFGMDNYCDAINNRAFCNYDGDGCTSTVTKTKVPPFMSCDLQDGCARD 1610
QY 1785 PKAEN 1790
DB 1611 PQAGEH 1616

RESULT 11
US-10-741-600-1406
: Sequence 1406, Application US/10741600
: Publication No. US20050026189A1
: GENERAL INFORMATION:
: APPLICANT: CARGILL, Michele et al.
: TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
: TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
: FILE REFERENCE: C1001499
: CURRENT APPLICATION NUMBER: US/10/741,600
: NUMBER OF SEQ ID NOS: 73997
: SOFTWARE: FASTSEQ for Windows Version 4.0
: SEQ ID NO 1406
: LENGTH: 1627
: TYPE: PRT
: ORGANISM: Homo sapiens
US-10-741-600-1406

Query Match      39.7%; Score 3916.5; DB 17; Length 1627;
Best Local Similarity 45.8%; Pred. No. 1.3e-289;
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

QY 249 REAETFSQVGLP--ILYFSGRRL--LRLPEVLAIEIPRAFTVEAWKPGGONPAII 305
DB 80 REARGATEBSPSRALYFSGRGEQLRLRADL--ELPRDAFTLQVWLRAEGGQSRPAVI 137

```

QY	306	AGVPDNCHTYS	DKCMALGISGCKGRDARF	PSFLCTDPRVKATIL	ISHSRQPGW	365																																															
Db	138	TGLYDKCSYIS	RDRGMVVG	IHTISDQDKDP	PPYFSLTDRARQYTT	INARSYLPGWV 197																																															
QY	366	HVAATYDGR	HMALYDTQT	OVASSLDQSP	LNSPFMA	CRSLLLGGDSSE	DHYFPGHGT 425																																														
Db	198	YLAATYDQ	PFKLYNGA	OVATISG	QVIGISPLQ	KCYLMLGG--SALHNH	RGYIEH 255																																														
QY	426	LVMSTALP	QSHFQHS	SGHSSG	SEEBATDVL	TASFEVNT	WVPFRDEKYP	RLLEV--LOG 483																																													
Db	256	FSLMVART	OREBELL	ISMDETH	GAHTLPOLL	LOEMDN	VKHAMSPK	DGSSPKVEFS	NAHG 315																																												
QY	484	FEPEBELL	SPLOP	RCGQ	TCVDN	VELISQ	YNGYWL	REBEXI	RAYOVN	ICDEGL	NIVS 543																																										
Db	316	FLLD---	TSLEP	PLCGQ	TLC	DNTE	VLASYNQ	LSFRQ	PKVVRK	VALL	YEDDHKN	PNVT 371																																									
QY	544	EEQILR	QHEALNEA	RSRYNIS	SMQ	LSVHVN	STLHR	VLVNC	BEPS	SKGN	DHCE	PECEHP 603																																									
Db	372	REQVD	FOHOLA	EA	KOYNI	SMELD	VL	EVNS	SLRR	ILIAN	CDLSK	IGDEN	CECHNT 431																																								
QY	604	LTYDGD	DCR--LQGR	CYS	MNR	RDGL	CHVE	CNN	MLN	PDGD	CCDP	QVAD	VARKTC	CFDPSP 662																																							
Db	432	LTHGDG	DCRHLR	HPA	FAV	KQGN	GV	CDMD	CYNER	FN	PFQ	GE	CCDP	ELIN	YTQ	CFDPSP 491																																					
QY	663	KRAYSV	VELKEAL	OLN	STH	PLNT	PLNT	PLNT	PLNT	PLNT	PLNT	PLNT	PLNT	PLNT	PLNT	PLNT 722																																					
Db	492	HRA	YAD	VEL	KNL	IL	LD	ST	HLN	TL	FFA	S	SEEL	AG	VATW	PD	KAL	MHL	LG	IV	LN	PSFY 551																															
QY	723	GMPGH	TD	IM	HE	VG	VL	GL	YH	FK	VS	RS	ES	EN	D	CKE	TV	S	ME	GD	CA	DTA	P	PKSEL 782																													
Db	552	GMPGH	TH	IM	HE	IG	SL	GL	YH	FK	VS	RS	ES	EN	D	CKE	TV	S	ME	GD	CA	DTA	P	PKSEL 611																													
QY	783	CR	BE	PT	SD	TC	GF	TR	PG	A	P	T	N	M	S	Y	T	D	N	C	T	D	N	F	T	P	N	O	V	A	R	M	C	Y	L	D	V	Y	O	Q	M	T	ES	RK 842									
Db	612	CGD	PE	R	G	N	D	T	C	GF	H	S	F	F	N	T	P	N	N	F	M	S	Y	A	D	D	C	T	D	T	C	B	F	N	O	V	A	R	M	C	Y	L	D	V	Y	O	Q	M	T	ES	RK 671		
QY	843	P	T	P	I	P	M	V	I	G	O	N	K	S	L	I	T	H	M	P	I	S	G	V	Y	I	D	R	A	S	G	S	I	C	A	C	A	E	B	T	E	G	T	R	O	Y	N	H	A	S	S	R	V 902
Db	672	P	A	P	V	A	L	A	O	V	I	G	H	T	D	S	V	T	L	E	M	P	I	D	H	F	E	R	E	L	G	S	A	C	H	L	E	R	I	L	V	O	A	S	N	A	S	M	P 731				
QY	903	C	D	S	G	S	Y	M	P	E	A	V	G	P	D	V	O	P	C	E	P	E	L	A	M	S	P	V	N	L	H	N	M	T	P	C	P	C	--T	E	G	S	L	E	L	L	F	O	H	P	V 961		
Db	732	C	S	P	S	G	M	S	P	R	E	A	G	P	D	V	O	P	C	E	P	E	L	A	M	S	P	V	N	L	H	N	M	T	P	C	P	C	--T	E	G	S	L	E	L	L	F	O	H	P	V 791		
QY	962	Q	A	D	T	L	L	W	T	--S	F	E	M	E	S	S	O	V	L	F	D	E	I	L	L	E	N	K	S	A	H	L	E	P	L	T	C	D	I	P	L	T	K	L	--H	V	D	K	Y	S 1018			
Db	792	V	P	E	S	T	L	I	W	T	P	S	T	M	D	S	S	A	N	D	I	K	L	A	V	S	K	N	I	S	L	O	P	W	F	C	O	V	P	L	I	L	M	D	G	E	E	V 851					
QY	1019	G	V	K	O	V	T	D	E	R	I	E	A	L	I	T	S	O	P	H	S	L	C	S	G	R																											

[illegible]

```

Db 316 FLND-----TSLERPLCGQTLCDNTEVIAASYNQJSSFPQKVVYRVVNLVEDHKNFVT 371
Qy 544 BEQRILOHEALNAEFSRYNISWQLSVHQNSTLRHRVTVLNCPSKIGNDHCDPECBHP 603
Db 372 REQVDFQHQLABAFKQYINISWELDVLEVSNSSLRRLILANCOISIKIGENCDPECNHT 431
Qy 604 LTGYDGDGDCR-LQGRCSVMNRBDGLCHVECNMNLNDDDDGCCDPOVADYRKTCPDPS 662
Db 432 LTGHGGDCCHLRPAFVKQKOHNGVCDMDCYERKFNPDGGECDPELTNTVQTCFDPDSR 491
Qy 663 KRAYMSYKELKEALQNLSTHPLNTYFASVYEDLAGATWPMWDXOATYHGLGIVLSPAY 722
Db 492 HRAYLVNLEKNILKLDGSTHLNIFPAKSSSEELAGATWPMWDXOALHGLGIVLANSFY 551
Qy 723 GMRGHTDMHEVGHVGLYHVFVGSBRSCNDPCKEYVSMETGOLCADTAPRYSEL 782
Db 552 GMRGHTMTMHEIGHSLGLYHVFGRISBIOCSDPCHMETEPRFETGOLCNDTNPAKGS 611
Qy 783 CREBEPTDTCGFRFPAGPPTNMYSTDDNCTDNFTPNQVARMHCYLDLVYQOQWTSRK 842
Db 612 CGDPRGNDTCGRHSFNTPTNNMSTADDOCTDFTPNQVARMHCYLDLVYQOQWTSRK 671
Qy 843 PTPRIPMYIGQTNKSLITHTMLPRISGVYVDRASGSLCGACTEDGTFRQYVHTASSRV 902
Db 672 PAPVALAPVLGHTTDSVTLFMPRIIDGHPFERELGSACHLCLEGRILVQYASASSPMP 731
Qy 903 CDSGTYTPREBAGRPVVDQPCERPSLOAMSBEVHLVNMNTVPCR-TEGCSLEILFQHPV 961
Db 732 CDSGTHMSPREABCHPVEQPCSKSVRTWSPNSLVNHTVPACPREQGCYLELEFLYPL 791
Qy 962 QADPLTLMTV--SPFMSSQVLPETELLENKESVHGLDPTFCDILTKL-HVDKVS 1018
Db 792 VPESLITWTFVSTWDMDSGAVNDIKLLAVSGKISJAPQVNFCDVPLTRLMDVGEVY 851
Qy 1019 GVKYVTERDEIIDAALLTSQPSPLCSGCRPVAYQVLRDPPFASGIPVVTSHSRKFTD 1078
Db 852 GIQIYTLDEHLEIDAAMLTSTADTLPCLQCKPLKYKVRDPLMDVASTLI-HMKRFVD 910
Qy 1079 VEVTFGOMYQVQLABAGSELGEASPLNHNHGAHYCGDGKVSRLGECDDGDVSGDG 1138
Db 911 MDNLGSGVYQVWYTTISGTESESPSPAVTYIHGRGYCGDGIQDQGEQCDMDMKINGDG 970
Qy 1139 CSKVCLEBEGFNCGEBSLCTMYGSGDGCICRPEBKTSIVOCIGTIPKGYLDQWATRAVS 1198
Db 971 CSJLPCROEVSFNCIDEBRSRCPFHGDGVCBEFEGKTSIKOCGVYTPGDLQWMSNVS 1030
Qy 1199 HEDKKCPVSLVTGER-HSLICTSYHPLDPMHRLTPMPCVASENETODDRSBEPSGL 1257
Db 1031 HQD-QQCRGMVITIGPRAASQVCRKTVIDLSEGISQHAMVCTTISYPSQ----- 1078
Qy 1258 KKEDEVMLKVCENRGEARAIFFLTJTDGLVGEHQPTVTLVLTDVRSNHSIGTYGLS 1317
Db 1079 LAOTTFMLRAVFSQPMVAALVIVLVDGYGQKQKETSIVOLDJTKDQSHDGLHVLVS 1138
Qy 1318 CONNPLIINTHHQNVLFHHTTSVILNFSRPRVIGISVALRTSRIGLSRPNCSISDEG 1377
Db 1139 CRNNPLIIPVHDLISQFHYHQAARVSFSSPLVAISGALRSFDPNDPVTLLSSC-QRGFT 1197
Qy 1378 QNHQOGSCIRHPCGKODSCPSLLDHDVNVCTSI-----GPGLMKCAITGORGALQASS 1433
Db 1198 YSAPASGCVFACBKTD-CPELAVENAS-LNCSSTDHYG---AQCTVSCRTGVLDQIR 1252
Qy 1434 GQYIRPMQ--KEILLTSSGHWONVSCLPVDCGVDPSPSLVNTANFSGSGTFLKRCST 1491
Db 1253 DDELIKSQTPSVYVCTTECKMKMKQVACEPVDCSIPIHQYUASFSFCPGTFTGSGCSF 1312
Qy 1492 SCVPRAPOGLSPMLTCLDEGLMSLBEVYCKLEBDAPILNLNMLLPHLCQDNHVTI 1551
Db 1313 QCHHPOLKNNNSLTLTMEGLWSFPALCEMLAPRVPVNNADLQIARCRENHGKGSF 1372
Qy 1552 CKTECKRGYVVAASBEGVANKLLKIQLEGGIIEGQSCIPVVECPRPVFEKGVECTNG 1611
Db 1373 CKTKCKRGYVHPGSSR-KSKKRAFKTQCTQDGSQWBAQVYVTCDDPPRFHGLYQCTNG 1431

```

```

Qy 1612 FSLDSQVLANC-----NOERBKLPILCTKEGLWQBEKLCENLOGECPPEPSLNS-VBY 1665
Db 1432 FQFNSBGRICEDSDASQGLGSNVYHCRKQDGNWSFHVQOEQOGC-SVFNELNSMLKL 1490
Qy 1666 KCEQYIGIAGVCSPLCYIPSPDPVMLPENITADTLBHMMEPVKQSVYCTGRQWHPDPV 1725
Db 1491 QCPRGVATGSEBACTSCIDHNSBSIILPMNTVARDIPMLNPTKRYKRVCTGLKMYHFA 1550
Qy 1726 LVHICQSCERPQADGWCMTINNRAVCHYDGDCCSSTLSKRVLPFAADCDL-ECTCRD 1784
Db 1551 LHVCKCEPFGMDNYCDALNNRAFCNYDGDCCSTVTKTKVYFPFMSCDLQGDACARD 1610
Qy 1785 PKAEN 1790
Db 1611 FOAQB 1616

RESULT 13
US-10-887-229A-8
; Sequence 8, Application US/10887229A
; Publication No. US20050148509A1
; GENERAL INFORMATION:
; APPLICANT: DAKE, BRIAN
; APPLICANT: BOOTH, BARBARA
; APPLICANT: BOES, MARY
; APPLICANT: BAR, ROBERT S.
; TITLE OF INVENTION: BINDING PROTEINS AS CHEMOTHERAPY
; FILE REFERENCE: IOWA:049US
; CURRENT APPLICATION NUMBER: US/10/887,229A
; CURRENT FILING DATE: 2004-07-08
; PRIOR APPLICATION NUMBER: 60/538,000
; PRIOR FILING DATE: 2004-01-21
; PRIOR APPLICATION NUMBER: 60/485,846
; PRIOR FILING DATE: 2003-07-09
; NUMBER OF SEQ ID NOS: 16
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 8
; LENGTH: 1627
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-887-229A-8

Query Match 39.7%; Score 3916.5; DB 18; Length 1627;
Best Local Similarity 45.8%; Pred. No. 1.3e-289;
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

Qy 249 REAETFSQVGLP--ILYFSGRERL-LLRPVLAETPREAFVYEAWKEGCONPAIT 305
Db 80 REARGATEEPPSPSRALYFSGRQBQLRVLRADL--ELPRDAFTLQVLRABGGQSRPAVI 137
Qy 306 AGVFDCNSHTVSDKGMALGIRSGDKGKRDARFPFSLCTDRVKKATLLISHRYQPTWT 365
Db 138 TGLYDKCSYISRDGRWVYGHITISDQDNKOPRYFFSLKTRARQVTTINHRASYLPQWV 197
Qy 366 HVAATTDGRMALVYDGTQVASSLDQSGPLNSFPMASCSLLGCGSSBEGHYFRGLGT 425
Db 198 YLAATYDQGFPMKLYNGAQVATSGEYVGIFSLTQCKVLMLOG--SALNHNRYGIEH 255
Qy 426 LVFMSTALPQSHRQHSQHSQSGEEAATDVLTLTASFEPVNTWEPFRDEKPRLEV--LOG 483
Db 256 FSLMKYAKTQRELISDMETGANTALPQLLQENWDMVKRAMSMDGSSPKVFEFSNAG 315
Qy 484 FEPEBILSPQLCGQTVCDNVELISQYNGWYPLRGEKVIYYQVNIICDQGLNPIVS 543
Db 316 FLND-----TSLERPLCGQTLCDNTEVIAASYNQJSSFPQKVVYRVVNLVEDHKNFVT 371
Qy 544 BEQRILOHEALNAEFSRYNISWQLSVHQNSTLRHRVTVLNCPSKIGNDHCDPECBHP 603
Db 372 REQVDFQHQLABAFKQYINISWELDVLEVSNSSLRRLILANCOISIKIGENCDPECNHT 431
Qy 604 LTGYDGDGDCR-LQGRCSVMNRBDGLCHVECNMNLNDDDDGCCDPOVADYRKTCPDPS 662

```

```
Dh 432 LTGHGDDGCRHLRHFAFKQHNHGVCDMCDYERFNFDEGCECDPEITNTVYTCFCFDDSP 491
Qy 663 KRAYMSXKEIKELQNLSTHFLNLYFASVREDLAGAATWPMWDATATHIGIYLSPAY 722
Dh 492 HRAYLDVNEIKNLKLDGSTHLNLFKASSBEEBLAGATWPMWDEALMLGGIYLNISFY 551
Qy 723 GMEGHTDMHEVGHVGLYHVFKEGVSERSCNDPCKETVPSMETGDLCAJTAFTPKSEL 782
Dh 552 GMEGHTMTMHEIGHSGLYHVFKEGVSERSCNDPCKETVPSMETGDLCAJTAFTPKSEL 611
Qy 783 CREBEPISDTGCTFRFGAPFTNTMYSTDNDCTDNFIPNOYARAHCTLDLYOQWTSRK 842
Dh 612 CGDPGPNDDTCGFHSFNTPTNNFMSYADDCTDSFTPNQYARAHCTLDLYOQWTSRK 671
Qy 843 PTPRIPRMVIGQNKSLTIHMLPRISGVVYDRASSGLCGACTEDGTFROYVTHASSRV 902
Dh 672 PAPALAPOLYAGHTDSTLWEMFPIIDGHFERELSGACHLCGRIILVOJANASSPMP 731
Qy 903 CDSGYWTPREAVGPPVDPOCEPSILOAMSPVHLYMMNTVPCP-TEGSGLELFPQPV 961
Dh 732 CSPSGHMSPREABGHPRVBOCKSSVATWSPNSAVNHTVPACRPEOGCYLEFLIYPL 791
Qy 962 QADTLTLMWT--SEFMSSOVLPELTILLNKESVHLGRLDTCDFIDLYTKL-HVDGVS 1018
Dh 792 VPBSLITWTFVSTDMDSGAVNDIKLAVSGKNIISGPOVFCDFVPLTIRLMDVGEVY 851
Qy 1019 GVAVYTFDELEIDALLTSOPHSPLCSGCRPVAYOULRDPFPASGLPVVYTHSHRKFTD 1078
Dh 852 GIGYTLDELEIDANALSTADTPLCLQCKPLKVVARDPLOMDASTIL-HLNKRFVD 910
Qy 1079 VEYTPGQMYOYVLAEBAGELGEASPRYLNIHGARYCGDGKVSERLEECDDGDLVSGD 1138
Dh 911 MDNLGVSUYWVITITIGTESEBSPRAYTIHGRGYGDDGIQDQGEQCDMDMKINIGD 970
Qy 1139 CSKYCELEBEGNCGYBPSLCYMEEGDGI CEFPERKTSI VDCGYTPRGYLDQMATYSS 1198
Dh 971 CSJFCRQEVFNFCIDEPSCRYCFYHGDGVCEFEOKTSIKDCGVYTPGFLDOWASNASVS 1030
Qy 1199 HEDEKKKQVSLVTGER-HSLICTSYHNDLPMHRPLTMPCPVASENTEODDRSQRPGSL 1257
Dh 1031 HQD-QQCPGMYITIGOPASQVCRKTVIDLSEGISQHAMYPPTTISYPSQ----- 1078
Qy 1258 KKEDEWMLKVCFNPRGEARAFIFLTTDGLVGEHQPTVLYLTDVRSNHSIGTYGLS 1317
Dh 1079 LAQTFMLRAYFSQPMVAAYIVHLVDTGYGQKQETISVGLDTRKQSHDLGLHYLS 1138
Qy 1318 COHNPLIINTTHQNLPHRTTSVLANPSSPRVIGISAVALTSTRIGLSAPNSCISDEG 1377
Dh 1139 CRNNPLIIPVHDSQPFYHSQAVRVSFSSPLVAISGVALRSPDNFPTVLTSSC-QRGET 1197
Qy 1378 QNHQSGSCIRPCGKODSCSILLDHADVNCSTI-----GPGMLKCAITCORGALQASS 1433
Dh 1198 YSPABQSCVPRACKTD-CBELAVENAS-LNCSSTDRTYG--AQTVCSCRTGYVLDIR 1252
Qy 1434 GOYIRPQO--KEILLTSSGMDQNVASCLPYDCVPPPSLVNANFSCSBGTKEKLCST 1491
Dh 1253 DDELIKQOTGVSIVLTCTBEKMNQVACBPVDCSIRPHNQVYASFCSPGTTGSGCSF 1312
Qy 1492 SCVPRAKQIGSPMLTCLIEDGLMSLPVYCYKLECDARPIIANMLPHCLQDNHDYGTI 1551
Dh 1313 QCRHPAOLKGNNSLLTCTMEGLWMSFPBALCELMCLAPRPVADLQTPARCEMNGKXGSF 1372
Qy 1552 CKYCECKGYVVAASABEKVNRKLIKICLBEGIWEQSGCI PVCEPAPPVPEGYECNNG 1611
Dh 1373 CKKCKCKGYHVGSSR-KSKRAFKTCTODGSMQOBACVAVTCDPPPKFHGLYQCTNG 1431
Qy 1612 FSDISQCVLNC-----NOERKPLPILCTKEGLMTQEFKLCENLOGECPRPSELSN-VXY 1665
Dh 1432 FQFRSEBRICEDBDASQIGSNVIHCRKQCTWNGSHVQCEMGOQO-SVPNELNSMLKL 1490
Qy 1666 KCBOGYIGAVCSPLCVIPSPDVMPLBENITADTLEHMEBVKYQSICTGCRROMHPDV 1725
Dh 1491 QCPBGVAIGSECATSCIDHNSESIIILPMNVTVRDIPIHMLPTVERVYVCTAGLKMYPHA 1550
```

```
Qy 1726 LVHACISCEPQADGWCDTIRNNRAYCHYDGDCCSSLSKKEYIPRAADCDLDELCTCRD 1784
Dh 1551 LHCYVAGCEPFPMDNDYCDALNNRPAFCNDYGDGDCCTSTVTKKYVTPFPMSCDLGDGACRFD 1610
Qy 1785 PKAEN 1790
Dh 1611 POAEN 1616

RESULT 14
US-10-783-311-2
; Sequence 2, Application US/10783311
; Publication No. US20050009136A1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; APPLICANT: Hogan, Shannon
; TITLE OF INVENTION: PAP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783,311
; PRIOR FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448,515
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 1547
; TYPE: PRF
; ORGANISM: Homo sapiens
US-10-783-311-2

Query Match 39.7%; Score 3914.5; DB 17; Length 1547;
Best Local Similarity 46.1%; Pred. No. 1,7e-289;
Matches 714; Conservative 295; Mismatches 490; Indels 51; Gaps 24;

Qy 263 LYFSGRERRI-LIRPEVLAIPREDAFTVEAWKREBGQNNPAILIAGYFDCSHTVSDKGM 321
Dh 16 LYFSGRGEQRLVRADL--ELPRDAFTLQWMLRABGQRRSPAVITGLYDCSYISRDGM 73
Qy 322 ALGIRSGDKRDAPEFSLCTDRVKKATILLSHSRYOGCTWTHVATYDGRHMLYVD 381
Dh 74 VVGHTISDDNDNDPRFFESLKTDRARQVTTINAHNSYLRPGOWYLAATYLDGQPMKLYVN 133
Qy 382 GTQVASSLDGSLNPSFMAASCSLLLGSDSBDGHYFRGLTLYVWSTALPQSHFQHS 441
Dh 134 GAQVATSGEQVGFSPRLQKCKVLMCG--SALNHVRYGVIHFSLMKVARTQREILSD 191
Qy 442 SQHSSGEEATDVLTRASPEPVNTWYPRFDEKYLEV--LOGFEBEPLISPLQEPIC 499
Dh 192 METHGANTLPLOLLQEMNDNVGHAMS PMKDGSSPKVEFSNAGFLD---TSLRPLC 247
Qy 500 GQTVCONVELISQYNGWPLRGEKVIRYOVVNICDEBGLPPIVSEQIRLQHEALNFAFS 559
Dh 248 GQTLCDNTEVYASYNQLSFRQKRVKRYVNLVEDDHKPIYTRQVYDQHNQLEAFK 307
Qy 560 RYVISMQLSYHOVANGSTLRHVVLVNCEPSKIGNDHCPRECEHPLTGYDGDCR-LOGRC 618
Dh 308 QYNSWELDYLEVNSSLRRRLILANDDISKIDBENDCPCHNTLTCGHDGDCRHLRHPA 367
Qy 619 YSNRRDGLCHVECNMNLDFDDGCCDPADVARKTCFPRDPSPKRAYMSXKEIKELQOL 678
Dh 368 FVKQKHNGVCDMCCNERFNFDEGCECDPEITNTVYTCFCPDPSPHRAVLDVNEIKNLTKL 427
Qy 679 NSTHFLNTYFASVREDLAGAATWPMWDKAVNTHLGGIVLSPAYYGMGHTDTMHEVGHV 738
Dh 428 DGSHTNLIFPAKSSBEEBLAGVATWPMWDEALMLGGIYLNISFYGMGHTMTMHEIGHSG 487
Qy 739 LGLYHVFKEGVSERSCNDPCKETVPSMETGDLCAJTAFTPKSELCREBEPISDTGCTFRF 798
Dh 488 LGLYHVFKEGVSERSCNDPCKETVPSMETGDLCAJTAFTPKSELCREBEPISDTGCTFRF 547
Qy 799 PGPFTNYSYTDNCTDNFTPNQVARMHCYLDLYOQWTSRKPTPIPRPVYIGQTNK 858
```

Db 548 FNTFNNFMSYADDDCTDFTPNQVARMHCYLDLYQGMQSRKAPVALAQLVGLHTTD 607
 Qy 859 SLTIHMLPPIGUVVYDASGSLCGACTEDGTFROYHTASSRRVCDSSGYTPPEAVGP 918
 Db 608 SVTLEMPPIIDGHFERELSGACHLCLEGRILVQASNASSPMPSCPSGHSMPREAGHP 667
 Qy 919 DVQOPCEPSLOAMREVLHYHMMNTVPCR-TEGSELELPHQVADTLTLMVT--SPFM 975
 Db 668 DVEOPCEPSVTRMSPNSAVNPHVTPRACPEOGCYLELEPLVPLPESLTIWTFVSTDW 727
 Qy 976 ESSQVLFTEILLLENKESVHLGRLDTPCDLPLTIKL-HVDSKVSQVKVYTFDERIEIDAA 1034
 Db 728 DSSGAVNDIKLAVSGNKISLGPQNVFCDFVLTIRLMDVGEVYGIQIYTLDEHLEIDAA 787
 Qy 1035 LITSQPSPLSCGCRPVRYOVLDRPPFASGLPVVVTSHKRTVEVTPGCMYOVLAE 1094
 Db 788 MLTSTADTPLCLOCKPLKXKVVDRPLOMDVASIL-HLNRFVMDMLNGSVYQYWTYTI 846
 Qy 1095 AGGELGASPRPLNHGAPYCGDKVSRLEGECDODDLYSGDGSKYCELEBEPNCVE 1154
 Db 847 SGTEESPSPAVVYTIHGRGYCGDGIQKDGEGCCDDMKKINGDCSLFCRQSVFNCIDE 906
 Qy 1155 PSICYMEGDGICERPERKTSIVDCGIYTPKGYLDQWATRAYSSHEBKCKPVLVTGER 1214
 Db 907 PSRCYFHSDGVCSEFEBOKTSIKDCGYTTPOGFLDQASNASVSHQD-QQCGWVITIGQ 965
 Qy 1215 -HSLICTSYHPRDLNHRPLTGMFPCVASENETQDRSEQREGLKKEDEVMLKVCFNRP 1273
 Db 966 AASQVCTKTYDLSEGISQHMVPTCTISYPYSQ-----LAQTFMLRAYFSGPM 1014
 Qy 1274 EARAIFLPLTDDGLVPEHQOPTYTLVLTLYVRSNHSIGTYGLSCONNPLINTHTQNV 1333
 Db 1015 VAAAVIYHVLVDGYTDQOKETISVQLDLDKQSHDGLVLSCRNNPLIIPVHDLQ 1074
 Qy 1334 LFNHTTVLNLNFSRPVIGISAVALTSTSRIGLSAPNSCISEDEGONHOGOSCHIRPCGQ 1393
 Db 1075 PFIHSQAVRVSFSPPLVAISGVALRSFDNPRVLTSSC-ORGETYSPAESCVHFACEKT 1133
 Qy 1394 DSCPSLLLDHADVNVCTSI-----GRLMKCAITQORGFALQASSGOYIRPMQ--KEILLT 1447
 Db 1134 D-CPELAVENAS-LNCSSSDRYHG---AQCTVSCRTGVLDIRRDELKISQGTSPVTVT 1188
 Qy 1448 CSSGHNQONVCLPVDGCVPRPRLVNYANFSGSCTKFLKRGCSISCPYPALQGLSFWLT 1507
 Db 1189 CTBEKMKQYQACEVDVDSIPRHHQVYASFCRPGITTFGSGCSFQCRHPALCKNNLSLT 1248
 Qy 1508 CLEBDGLSLPEVYCKLECDAPRIILNANLLPHCLQDNHVDGTICKTECKRGYVVAESAB 1567
 Db 1249 CMEDGLMSFEBALCELMCLAPRPVPAADLQYARCKRNKHKVGSFCKTKCKRGYHVPSSR 1308
 Qy 1568 GKVRNKLKLIQCLEGGIWEQSCIPVVCERPPEVFEQVETCTNGFSLDSQCVLNC----- 1622
 Db 1309 -KSKRAFKYQCTQDGSQWQSBACVPTCDPRPRFHLGYOCTNGFQNSBECRICEDSDA 1367
 Qy 1623 NOBEREKPIILCTKEGLTQEFKLCENTOGBCRPPPSBLNS-VEXKCEOGIGTAVCSPLC 1661
 Db 1368 SOGLGNSVNHICRKGQGNKGSFHYQCEMOQOC-SVYNELNSNLKIQCDPQYVIGSECATSC 1426
 Qy 1682 VIPSPDVMPLPENTADTLEHMEPVKYOSVCTGRGROMHPDPLVHVCIOSCEPFOADGW 1741
 Db 1427 LDHNSSEIILPANTVYDIPMLNPTVERVYCTAGLKWPHRPLHICVAGCEPFGMDNY 1486
 Qy 1742 CDTINNRAYCHYDGDCCSSTLSASKVILPRAADCLD-ECTCRDPKAEEN 1790
 Db 1487 CDAINNRAPFCVYDGDCTGTVTKTKVTPFPMSCDLQGDACRDPQAOEH 1536

RESULT 15
 US-10-741-600-1403
 ; Sequence 1403, Application US/10741600
 ; Publication No. US20050026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.

; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; TITLE OF INVENTION: MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 ; FILE REFERENCE: C0001499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: PasteSeq for Windows Version 4.0
 ; SEQ ID NO 1403
 ; LENGTH: 1420
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-741-600-1403
 Query Match 36.5%; Score 3602; DB 17; Length 1420;
 Best Local Similarity 45.9%; Pred. No. 1,26-265;
 Matches 659; Conservative 269; Mismatches 461; Indels 48; Gaps 22;
 Qy 376 MALVYDGYVASSLSDGSPINSPFMACSRSLILGSDSSDGHVFRGHGLTVLFWSTALPQ 435
 Db 1 MCLVYNAQVATSGEYGVGIFSPITQCKCYLMLGG--SALNHNYRGYIEHNSLKVARTQ 58
 Qy 436 SHFQHSQHSGBEATDVLVLTASFEPVNTWVPREDEKYPRLEV--LQGFEPREILSP 493
 Db 59 RELSDMETHGANTALPQLLQENWMDVVKAMSPKXGSSPKVFNHAGFLD-----TS 114
 Qy 494 LQPPLCQGYICDVELISQYNGVYPLRGEKYIRQVYVNICDDEGLNPVSEBOIRLQHEA 553
 Db 115 LEPLCGQITCDNTEVLASYNQLSSFPQPKVVRVYVNLVEDDKNPVTEEOVDFQHQ 174
 Qy 554 LNEAFSRVYNSWQLSYVQHNSTLRHRVVLVNCPSRXIGNDHCPECEHPLTGYDGGCR 613
 Db 175 LAENFKQYNSWELVDLEVSNSLRRLILANCDISKIGDENCPCECHNTLTGHDDGR 234
 Qy 614 -LQGRCYSMNRBDLCVHECNMNLNDEPDGDCDPOVADYAKTCFDPDPSPKRAYMSVKE 672
 Db 235 HLRRPAPVKKHNGVCMDCYERFNFDDGSCDPRZITNVYQTEFDPDPSPRAYLDVVEL 294
 Qy 673 KEALQNLSTHPLNYTPFASVREDLAGAATPMDQAVTHLGLYLSPAYGMPCGHTPMI 732
 Db 295 KNILKLDGSHLNLFFPKSSBEEELAGVATPMDKEALMHLGLIYLNPSFYCMPGHTPMI 354
 Qy 733 HEVGHVLYHVPFVGBERSCNDRCKEYVSMETGDLCAOTAPTPKSELCRBEPPTSOT 792
 Db 355 HEIGHSIGLYHVRGISEIQSCDPCMETEBSFETGDLCDNTNAPFKHKSAGDGFPGNDT 414
 Qy 793 CGFTFPFAGFTNYMSTYDNDCTDNFTPNQVARMHCYLDLYQGMQSRKAPVALAQLV 852
 Db 415 OGFHSFNTTYNNFMSYADDDCTDFTPNQVARMHCYLDLYQGMQSRKAPVALAQLV 474
 Qy 853 IGTNKSLLTIHMLPPIGUVVYDASGSLCGACTEDGTFROYHTASSRRVCDSSGYTP 912
 Db 475 LGHTTDDVTLEMPPIIDGHFERELSGACHLCLEGRILVQASNASSPMPSCPSGHSMP 534
 Qy 913 EAVGPRVDQPCESLOAMREVLHYHMMNTVPCR-TEGSELELPHQVADTLTLMVT 971
 Db 535 EABGHPVDEPCKSSVVTWSPNSAVNPHVTPRACPEOGCYLELEPLVPLPESLTIWTF 594
 Qy 972 --SEFMSSQVLFTEILLLENKESVHLGRLDTPCDLPLTIKL-HVDSKVSQVKVYTFDER 1028
 Db 595 FVSTDMSSGAVNDIKLAVSGNKISLGPQNVFCDFVLTIRLMDVGEVYGIQIYTLDEH 654
 Qy 1029 IEIDALLTSQPSPLSCGCRPVRYOVLDRPPFASGLPVVVTSHKRTVEVTPGCMYO 1088
 Db 655 LEIDAAMLTSTADTPLCLOCKPLKXKVVDRPLOMDVASIL-HLNRFVMDMLNGSVYQ 713
 Qy 1089 YQVLAEGELGASPRPLNHGAPYCGDKVSRLEGECDODDLYSGDGSKYCELEBEG 1148
 Db 714 YWVTTISGTEESPSPAVVYTIHGRGYCGDGIQKDGEGCCDDMKKINGDCSLFCRQSV 773
 Qy 1149 FNCVGEPSLCYMEGDGICERPERKTSIVDCGIYTPKGYLDQWATRAYSSHEBKCKPVS 1208
 Db 774 FNCIDBESRCYFHSDGVCSEFEBOKTSIKDCGYTTPOGFLDQASNASVSHQD-QQCGW 832

QY 1209 LVTGEP-HSLICTSYHBDLPNHRPLTGMFPCVASENETODDRSBOPEGLKKEDEWLVKV 1267
 Db 833 VIIGOPAAOYCRKTVIDLBSGISOHAMYPCTISYPSQ-----LAQTFMURA 881
 QY 1268 CFNRPGEARAIFLPLTDTGVLGEGHOQPTVTLVLTDVRSNHSIGTYGLSCQHNPLIINV 1327
 Db 882 YFSQPMVAAYIVLVTDTGYVDQKQETISVQLDTRKQSHDGLHVLSCRNNPLIIPV 941
 QY 1328 THHONVLFHHTTSVTLNPFSSRVRVISAVALRTSSRIGLSAPNSCISEDEQNHQOSCIH 1387
 Db 942 VHDISOPEYHSQAVRVSFSSPLVAISGVALSFDPNPVTLISC-QRGETYSPAEQSCVH 1000
 QY 1388 RPOGKODSPSILLDHADVVNCTSI---GPGLMKCAITCORGALQASSGQYIRPMQ-- 1441
 Db 1001 FACEKTD-CBELAVENA-YLNCSSSDRYHG---AQCTVSCRTGYVLQIRRDELIXQTG 1055
 QY 1442 KEILLTSSSGHMDONVSCLPVDCGVPDPSPSLVNVANFSCSEGTKFLKRCISCVPPAKLQG 1501
 Db 1056 PSYTVTCTEGKMNKQVACEPVDCSI PDHGYVAASFSCBEGTTFGSQCSFQCRHPAQLKG 1115
 QY 1502 LSPWLTGLELGLMGLPREVYCKLEBDAPRIIANLNLBPHCLQDNHDYGTICKVECKPGY 1561
 Db 1116 NNSLLTCEMEDGLWSFPBALCELMLCLAPPVPVNPADLOJARCRENKHVGSFCKYKCKPGYH 1175
 QY 1562 VAESAEGKVRNKLKIOCLEBGIWEOGSCI PVCEPPPVFEGMYECTNGFSLDSQCVLN 1621
 Db 1176 VPGSSR-KSKKRAKTKTOCTODGSMOEGACVPTCDPPPKHGLYXCTNGRQFNSBCRIK 1234
 QY 1622 C----NOERBKLPILCTKSGLWTOEFKLCENLQGECPPPPELINS-VEYKCEQYIGTA 1675
 Db 1235 CEDSDASQGLGSNVYHCRKDTGWSGPFVCOEMQGC-SVPELINSNLKLQCPDGYAIGS 1293
 QY 1676 VCSPLCVIPSPDPVMTADTLEHMEBVKQSVICTGRQRMHPDPVUHVCIQSCER 1735
 Db 1294 ECATSCLDHNSESIILPMNVTVRDI PHMLNPTVRVCTAGLKWYPHAPALIHCVKGCER 1353
 QY 1736 FOADGWCDTINNRAYCHYDGGDCSSTLSKVIIPAADCDLD-ECTCRDPKAEEN 1790
 Db 1354 FMGDNYCDALNNRAFCNYDGGDCCTSTVTKYKVTFFPMSCDLOGDCACRDPQAQEH 1409

Search completed: August 25, 2005, 22:29:33
 Job time : 141.279 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 22:17:11 ; Search time 26.5172 Seconds
(without alignment)

4385.960 Million cell updates/sec

Title: US-09-983-025B-2_COPY_234_1791

Perfect score: 8612

Sequence: 1 SPBESNONGEGSYRAET.....AADCDLDECTCRPKAEENQ 1558

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 7464964 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database :
- 1: Issued Patents AA:*
 - 2: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
 - 3: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
 - 4: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
 - 5: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
 - 6: /cgn2_6/ptodata/1/1aa/6C.COMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	8592	99.8	1791	4	US-09-827-998-3 Sequence 3, Appl
2	8263	95.9	1770	4	US-09-827-998-10 Sequence 10, Appl
3	6126	71.1	1385	4	US-09-827-998-16 Sequence 16, Appl
4	1709	19.8	717	4	US-09-949-016-9436 Sequence 9436, Ap
5	336.5	3.9	3594	4	US-09-911-842A-4 Sequence 4, Appl
6	330.5	3.8	3571	4	US-09-911-842A-2 Sequence 2, Appl
7	287.5	3.3	1847	6	5256642-10 Patent No. 5256642
8	287.5	3.3	1847	6	5472939-10 Patent No. 5472939
9	287.5	3.3	1847	6	5256642-10 Patent No. 5256642
10	287.5	3.3	1847	6	5472939-10 Patent No. 5472939
11	287.5	3.3	2039	6	5256642-2 Patent No. 5256642
12	287.5	3.3	2039	6	5472939-2 Patent No. 5472939
13	287.5	3.3	2039	6	5256642-2 Patent No. 5256642
14	287.5	3.3	2039	6	5472939-2 Patent No. 5472939
15	287.5	3.3	1947	4	US-09-612-314A-52 Sequence 52, Appl
16	284	3.3	2489	4	US-09-911-842A-5 Sequence 5, Appl
17	283	3.3	1466	6	5256642-6 Patent No. 5256642
18	283	3.3	1466	6	5472939-6 Patent No. 5472939
19	283	3.3	1466	6	5256642-6 Patent No. 5256642
20	283	3.3	1466	6	5472939-6 Patent No. 5472939
21	283	3.3	1537	6	5256642-5 Patent No. 5256642
22	283	3.3	1537	6	5472939-5 Patent No. 5472939
23	283	3.3	1537	6	5256642-5 Patent No. 5256642
24	283	3.3	1537	6	5472939-5 Patent No. 5472939
25	253.5	2.9	849	4	US-09-949-016-10271 Sequence 10271, A
26	249	2.9	830	1	US-08-110-158-4 Sequence 4, Appl
27	249	2.9	1033	4	US-09-834-309-1 Sequence 1, Appl

28	243.5	2.8	830	5	PCT-US91-05059-2	Sequence 2, Appl
29	236	2.7	577	2	US-08-435-149-3	Sequence 3, Appl
30	236	2.7	611	3	US-09-475-460A-32	Sequence 32, Appl
31	236	2.7	611	4	US-09-748-061A-32	Sequence 32, Appl
32	235.5	2.7	574	6	5378464-3	Patent No. 5378464
33	235.5	2.7	574	6	5378464-3	Patent No. 5378464
34	235	2.7	830	6	5378464-2	Patent No. 5378464
35	235	2.7	830	6	5378464-2	Patent No. 5378464
36	230.5	2.7	610	1	US-08-365-470-3	Sequence 3, Appl
37	230.5	2.7	610	3	US-09-209-668-19	Sequence 19, Appl
38	230.5	2.7	610	3	US-09-009-490A-89	Sequence 89, Appl
39	230.5	2.7	610	4	US-09-949-016-5942	Sequence 5942, Ap
40	230.5	2.7	610	6	5217870-2	Patent No. 5217870
41	230.5	2.7	610	6	5217870-2	Patent No. 5217870
42	230.5	2.7	647	4	US-09-949-016-10272	Sequence 10272, A
43	225	2.6	1394	4	US-09-949-016-5971	Sequence 5971, Ap
44	225	2.6	1394	6	5177197-30	Patent No. 5177197
45	225	2.6	1394	6	5177197-30	Patent No. 5177197

ALIGNMENTS

```
RESULT 1
US-09-827-998-3
Sequence 3, Application US/09827998
Patent No. 6656700
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
APPLICANT: Gu, Yizhong
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: NIHMPOR-8
CURRENT APPLICATION NUMBER: US/09/827, 998
PRIOR FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aeonica Sequence Listing Engine
SEQ ID NO 3
Patent No. 6656700
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-998-3

Query Match 99.8%; Score 8592; DB 4; Length 1791;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 155; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPBESNONGEGSYRAETFNQVGLPIFYSGRRRLRLRPEVLAIEPREAFTVEAMV 60
Db 234 SPBESNONGEGSYRAETFNQVGLPIFYSGRRRLRLRPEVLAIEPREAFTVEAMV 293
QY 61 KPBGQNNPAILIAGVPNGSHITVSDKMAIGISGKQKGRDARFFSLCTDRVKKATIL 120
Db 294 KPBGQNNPAILIAGVPNGSHITVSDKMAIGISGKQKGRDARFFSLCTDRVKKATIL 353
QY 121 ISHSRYQPGTWTHVAAATYDGRHMAIYDGTQVASSLDSQGPLNSPFMAACRSLLGGDSS 180
Db 354 ISHSRYQPGTWTHVAAATYDGRHMAIYDGTQVASSLDSQGPLNSPFMAACRSLLGGDSS 413
QY 181 EDGHPFRGHIGTLVFWSTALPOSHFQSSQHSQSGEAEATDLVLTASFEPTVTEWVPRDE 240
Db 414 EDGHPFRGHIGTLVFWSTALPOSHFQSSQHSQSGEAEATDLVLTASFEPTVTEWVPRDE 473
QY 241 KYRPLEVLOQFPEPEPRLSLPQLCCQTYCDNVELISQNGVWPLAGEKVIYQVNNIC 300
Db 474 KYRPLEVLOQFPEPEPRLSLPQLCCQTYCDNVELISQNGVWPLAGEKVIYQVNNIC 533
QY 301 DDEGLNIVVEEOIRLOHEALNEAFSRYSISWQSLSVQVHNSFTLRHVVVIVNCEPSKICGN 360
```

Db 534 DDEGLNPVISEEQLRLQHEALNEAFSRYNISWOLSVHVNSTLRHRVVLVNCPEPSKIGN 593
Qy 361 DHCPBCECHPLTGYDGGCRLQGRCYSMNRBDGLCHVECNMMLNDPDDGDCDDOVADVR 420
Db 594 DHCPBCECHPLTGYDGGCRLQGRCYSMNRBDGLCHVECNMMLNDPDDGDCDDOVADVR 653
Qy 421 KTCFDDPSPKRAYMSVKEALKEALQLNSTHPLNIFYASSVREDLAGAATWPKDXATVTHLG 480
Db 654 KTCFDDPSPKRAYMSVKEALKEALQLNSTHPLNIFYASSVREDLAGAATWPKDXATVTHLG 713
Qy 481 GIVLSPAYYGMGPHTDTMHEVGHVGLYHVFKGVSERESCNDPCKETVPSMETGDLCAD 540
Db 714 GIVLSPAYYGMGPHTDTMHEVGHVGLYHVFKGVSERESCNDPCKETVPSMETGDLCAD 773
Qy 541 TAPPKSELCEPEPTSDTCGFTPRPGAPFTNMSYTDNCTDFTFPQVARMHCYLDLV 600
Db 774 TAPPKSELCEPEPTSDTCGFTPRPGAPFTNMSYTDNCTDFTFPQVARMHCYLDLV 833
Qy 601 YQWMTESRKPPIPIPPVAVIGQTKSLTIHMLPPISGVVYDRASGSLCGACTEDGTFROY 660
Db 834 YQWMTESRKPPIPIPPVAVIGQTKSLTIHMLPPISGVVYDRASGSLCGACTEDGTFROY 893
Qy 661 VHTASSRRVCDSSGWTPEEAVGPPVDQCEPSLOAMSPEVHLYHMMMTVPCEPTEGCSL 720
Db 894 VHTASSRRVCDSSGWTPEEAVGPPVDQCEPSLOAMSPEVHLYHMMMTVPCEPTEGCSL 953
Qy 721 ELLOHNPQADTLTLMWTSFPMESSOVLFDTEILLNKESVHLGRLDPCDIPLTILKLV 780
Db 954 ELLOHNPQADTLTLMWTSFPMESSOVLFDTEILLNKESVHLGRLDPCDIPLTILKLV 1013
Qy 781 DGKVSQVAVYTFDEIRIEIDALLTSOPHSPLCSGCRPVRYOVLADPPASGLPVVYVTHSH 840
Db 1014 DGKVSQVAVYTFDEIRIEIDALLTSOPHSPLCSGCRPVRYOVLADPPASGLPVVYVTHSH 1073
Qy 841 RKFTDVEYTPQOMTQYOVLAAGBGLGEASPLNHHIGAPYCGDGKVSERLGECCDDGL 900
Db 1074 RKFTDVEYTPQOMTQYOVLAAGBGLGEASPLNHHIGAPYCGDGKVSERLGECCDDGL 1133
Qy 901 VSGGSCSVCELEBGFNCVGBRSPCYMYEGDICEPFRKTSIVDCGITYPKGYLDQWAT 960
Db 1134 VSGGSCSVCELEBGFNCVGBRSPCYMYEGDICEPFRKTSIVDCGITYPKGYLDQWAT 1193
Qy 961 RAYSSHEDKKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETQDRSEOP 1020
Db 1194 RAYSSHEDKKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETQDRSEOP 1253
Qy 1021 EGSJLKKEDEWLKYCFNRPGEARAIFFLTDTGLVPGHQOPVTLVLTIDVRGSHSLGT 1080
Db 1254 EGSJLKKEDEWLKYCFNRPGEARAIFFLTDTGLVPGHQOPVTLVLTIDVRGSHSLGT 1313
Qy 1081 YGLSCQHNPLIINTYHONVLFHHTTSVTLNFSRPGISAVLARTSRIGLSAPNSCIS 1140
Db 1314 YGLSCQHNPLIINTYHONVLFHHTTSVTLNFSRPGISAVLARTSRIGLSAPNSCIS 1373
Qy 1141 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNCTSIGFGLMKCAITTCORGFALQASS 1200
Db 1374 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNCTSIGFGLMKCAITTCORGFALQASS 1433
Qy 1201 GQYIRPQOKETILLTCSSGQMDQNSCLPVDGVPDPBSLVNANFSGBGTFKLKRCISIC 1260
Db 1434 GQYIRPQOKETILLTCSSGQMDQNSCLPVDGVPDPBSLVNANFSGBGTFKLKRCISIC 1493
Qy 1261 VPPAKLQGLSPWLCTLEDGLMSLPEVYCKLECDAPILILNANILLPHCLDNDHVGITCK 1320
Db 1494 VPPAKLQGLSPWLCTLEDGLMSLPEVYCKLECDAPILILNANILLPHCLDNDHVGITCK 1553
Qy 1321 YECKRQYVVAESABGKVRNKLKIQCLEGGIWEQSCIPVCEBPPPVFEGMTECTNGFS 1380
Db 1554 YECKRQYVVAESABGKVRNKLKIQCLEGGIWEQSCIPVCEBPPPVFEGMTECTNGFS 1613
Qy 1381 LDSQCVLNCNOERKPLPLCTYBGLMTQBFKLCENLQGBCCPPPSSELSNVSEYKCEQGYGI 1440
Db 1614 LDSQCVLNCNOERKPLPLCTYBGLMTQBFKLCENLQGBCCPPPSSELSNVSEYKCEQGYGI 1673

Qy 1441 GAVCSPLCVIPSPDPVWLPENITADTLEHMMEPKYQSIYCTGRQWHPPVLVHCIOQC 1500
Db 1674 GAVCSPLCVIPSPDPVWLPENITADTLEHMMEPKYQSIYCTGRQWHPPVLVHCIOQC 1733
Qy 1501 EPPQADGCDTINNRAVCHYDGDCCSSTLSKKVPIPPAADCDLDECTCRDPAEBNQ 1558
Db 1734 EPPQADGCDTINNRAVCHYDGDCCSSTLSKKVPIPPAADCDLDECTCRDPAEBNQ 1791

RESULT 2
US-09-827-998-10
; Sequence 10, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMRP-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecmica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 10
; LENGTH: 1770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-10

Query Match 95.9%; Score 8263; DB 4; Length 1770;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy 1 SPPEESNONGBESYBEAEFPNSOVGLPILYFSGRERLLRREVLAEIPREAFVTEAWY 60
Db 234 SPPEESNONGBESYBEAEFPNSOVGLPILYFSGRERLLRREVLAEIPREAFVTEAWY 293
Qy 61 KPBGQGNPPAILIGVFDNCSTHVSDDKGMALGIRSGDKGRDARFFPSLCTDVRKATIL 120
Db 294 KPBGQGNPPAILIGVFDNCSTHVSDDKGMALGIRSGDKGRDARFFPSLCTDVRKATIL 353
Qy 121 ISHSRYOPGTWTHVAAATYDGRHMAIYVDGTQVASSLDDSGPLNSPMAACRSILLGDDSS 180
Db 354 ISHSRYOPGTWTHVAAATYDGRHMAIYVDGTQVASSLDDSGPLNSPMAACRSILLGDDSS 413
Qy 181 EDGHYFRGHGTLVFWSTALPOSHFOHSSOHSGEAEATDVLVTASFEPVNTWVPFRDE 240
Db 414 EDGHYFRGHGTLVFWSTALPOSHFOHSSOHSGEAEATDVLVTASFEPVNTWVPFRDE 473
Qy 241 KYRRLVLOGFEBEPRIILSPLQPLCGQTYCNDVIELISQYNGWPLRGEKVIRYQVYVNIC 300
Db 474 KYRRLVLOGFEBEPRIILSPLQPLCGQTYCNDVIELISQYNGWPLRGEKVIRYQVYVNIC 533
Qy 301 DDEGLNPVISEEQLRLQHEALNEAFSRYNISWOLSVHVNSTLRHRVVLVNCPEPSKIGN 360
Db 534 DDEGLNPVISEEQLRLQHEALNEAFSRYNISWOLSVHVNSTLRHRVVLVNCPEPSKIGN 593
Qy 361 DHCPBCECHPLTGYDGGCRLQGRCYSMNRBDGLCHVECNMMLNDPDDGDCDDOVADVR 420
Db 594 DHCPBCECHPLTGYDGGCRLQGRCYSMNRBDGLCHVECNMMLNDPDDGDCDDOVADVR 653
Qy 421 KTCFDDPSPKRAYMSVKEALKEALQLNSTHPLNIFYASSVREDLAGAATWPKDXATVTHLG 480
Db 654 KTCFDDPSPKRAYMSVKEALKEALQLNSTHPLNIFYASSVREDLAGAATWPKDXATVTHLG 713
Qy 481 GIVLSPAYYGMGPHTDTMHEVGHVGLYHVFKGVSERESCNDPCKETVPSMETGDLCAD 540
Db 714 GIVLSPAYYGMGPHTDTMHEVGHVGLYHVFKGVSERESCNDPCKETVPSMETGDLCAD 773

```

QY 541 TAPTRKSELCREPPTSSTGCTGTRPGAPPTNMYSTDDNCTDNFTNOVARMHCIYDLV 600
DB 774 TAPTRKSELCREPPTSSTGCTGTRPGAPPTNMYSTDDNCTDNFTNOVARMHCIYDLV 833
QY 601 YQOWTESRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEGGTROY 660
DB 834 YQOWTESRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEGGTROY 893
QY 661 VHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSLQAMSPBVHL YHMMNTVPCTEGCSL 720
DB 894 VHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSLQAMSPBVHL YHMMNTVPCTEGCSL 953
QY 721 ELFFQHVQADTLTLMTSPFMESSQVLPDTEILLNKESVHLGRLPTFCIDPLITILKLV 780
DB 954 ELFFQHVQADTLTLMTSPFMESSQVLPDTEILLNKESVHLGRLPTFCIDPLITILKLV 1013
QY 781 DGKVGKVTYTFDERIEIDALLTSOPHSPICSGCRPVRYQVLRDPPASGLPVVYVTHSH 840
DB 1014 DGKVGKVTYTFDERIEIDALLTSOPHSPICSGCRPVRYQVLRDPPASGLPVVYVTHSH 1073
QY 841 RKFTDVEVTGQWYQVYVLAAGELGASBPPLNHIGAPYCGDKVSERLGECDDGDL 900
DB 1074 RKFTDVEVTGQWYQVYVLAAGELGASBPPLNHIGAPYCGDKVSERLGECDDGDL 1133
QY 901 VSGDGCRCVGELEGENCVCBPSCICYMEGDGICEPBERKTSIYDCGITYPKGYLDQWAT 960
DB 1134 VSGDGCRCVGELEGENCVCBPSCICYMEGDGICEPBERKTSIYDCGITYPKGYLDQWAT 1193
QY 961 RAYSSHDDKKKCPSLVTGEPHSLICTSYHNDLPNHPPLTGMPFPCVASENETODRSEOP 1020
DB 1194 RAYSSHDDKKKCPSLVTGEPHSLICTSYHNDLPNHPPLTGMPFPCVASENETODRSEOP 1253
QY 1021 EGSLLKEDVWLVKVCENRPGBARAIFIPLTTDGLVPBHQPTVTLVLTIDVRSNHSILGT 1080
DB 1254 EGSLLKEDVWLVKVCENRPGBARAIFIPLTTDGLVPBHQPTVTLVLTIDVRSNHSILGT 1313
QY 1081 YGSLSCQNPPLINTHQNVLPHHTTSVLFNSFPRIQISAVALRTSRIGLSAPNSCIS 1140
DB 1314 YGSLSCQNPPLINTHQNVLPHHTTSVLFNSFPRIQISAVALRTSRIGLSAPNSCIS 1373
QY 1141 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNVCTSIGPGLMKCAITOCRGFALQASS 1200
DB 1374 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNVCTSIGPGLMKCAITOCRGFALQASS 1433
QY 1201 GQYIRPQKEILLTCSGSHMDQVNSCLPVDGVPDPSPVLVNYANFSCSEGTKFLKRCISISC 1260
DB 1434 GQYIRPQKEILLTCSGSHMDQVNSCLPVDGVPDPSPVLVNYANFSCSEGTKFLKRCISISC 1493
QY 1261 VPPAKLOGSLPMLTCLBDGLMSLPBYVCKLECDAPRIILNANLLPHCLQDNHDVGTICK 1320
DB 1494 VPPAKLOGSLPMLTCLBDGLMSLPBYVCKLECDAPRIILNANLLPHCLQDNHDVGTICK 1553
QY 1321 YECRPGYVVAESAGKRNKLLKIQCLEGGIWEQSGSCIPVCEBPPEVFESEMECTNFGS 1380
DB 1554 YECRPGYVVAESAGKRNKLLKIQCLEGGIWEQSGSCIPVCEBPPEVFESEMECTNFGS 1613
QY 1381 LDSQCVLNCQERREKLPILCTKEGLMTQEFKLCENLQGECPPPPSBLNSVYKCEQGYGI 1440
DB 1614 LDSQCVLNCQERREKLPILCTKEGLMTQEFKLCENLQGECPPPPSBLNSVYKCEQGYGI 1673
QY 1441 GAVCSPLCVIPSPDPVMLPENITADTLEHNMPEVKQSIYCTGRQWHPDVLVHCIOQC 1500
DB 1674 GAVCSPLCVIPSPDPVMLPENITADTLEHNMPEVKQSIYCTGRQWHPDVLVHCIOQC 1733
QY 1501 E 1501
DB 1734 E 1734

```

RESULT 3
US-09-827-998-16
; Sequence 16, Application US/09827998

```

; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: NMORF-8
; CURRENT APPLICATION NUMBER: US/09/827, 998
; PRIOR FILING DATE: 2001-04-06/207, 456
; PRIOR APPLICATION NUMBER: US 60/207, 456
; PRIOR FILING DATE: 2000-05-26
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Acomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 16
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-827-998-16

```

```

Query Match 71.1%; Score 6126; DB 4; Length 1385;
Best Local Similarity 73.6%; Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 5; Indels 406; Gaps 1;

```

```

QY 1 SPPEESNQNGEGSYREAEITFNSQVGLPIYFGRRRLRLRPVLAETREATTVEAMV 60
DB 234 SPPEESNQNGEGSYREAEITFNSQVGLPIYFGRRRLRLRPVLAETREATTVEAMV 293
QY 61 KPEGGONNPAIINGVFNCSHTVSDKQWALGIRSGKDKGRDARFFSLCTDRYKATIL 120
DB 294 KPEGGONNPAIIL----- 306
QY 121 ISHRYQGTWTHVAATYDGRHNAALVYDGTQVASSLDQSGPLNSPFMAACRSLLLGDS 180
DB 307 ----- 306
QY 181 EDGHYFRGLGTLVFWSTALPQSHFQHSQHSQSGEEATDLVLTASFPVNTENVPRDE 240
DB 307 ----- 306
QY 241 KYRLRLVQGFPEPEILSLPPLQPLGQTVCDNVELISQYNGVWPLRGKVIYQVNNIC 300
DB 307 ----- 306
QY 301 DDEGLNPVSEEQIRLQHEALNEAFSRXNISWQLSYQVHNSLRLRVLVNCPEKXIGN 360
DB 307 ----- 306
QY 361 DHCDPECEHPLTGYDGDCLQGRCYSMNRDGLCHVECNMMLNDFDGDCCDQVADVR 420
DB 307 ----- 306
QY 421 KTCFPDPSKRAYMSVKELEALQINLSTHPLNTYFASVAREDLAAGATWPMDOAVTHLG 480
DB 307 -----G 307
QY 481 GIVLSPAYGMPGHTDTMIEHGVHVLGLYHVFQVSRRESNCPCKETVPSMETGDLCAD 540
DB 308 GIVLSPAYGMPGHTDTMIEHGVHVLGLYHVFQVSRRESNCPCKETVPSMETGDLCAD 547
QY 541 TAPTRKSELCREPPTSSTGCTGTRPGAPPTNMYSTDDNCTDNFTNOVARMHCIYDLV 600
DB 368 TAPTRKSELCREPPTSSTGCTGTRPGAPPTNMYSTDDNCTDNFTNOVARMHCIYDLV 427
QY 601 YQOWTESRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEGGTROY 660
DB 428 YQOWTESRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEGGTROY 487
QY 661 VHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSLQAMSPBVHL YHMMNTVPCTEGCSL 720
DB 488 VHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSLQAMSPBVHL YHMMNTVPCTEGCSL 547

```

```
QY 721 ELTFQHPVQADTLTLMWTSFFMESSQVLFDEIILENNKESVHLGPLDPCDIPLTIKLAHV 780
| | | | |
Db 548 ELTFQHPVQADTLTLMWTSFFMESSQVLFDEIILENNKESVHLGPLDPCDIPLTIKLAHV 607
QY 781 DGRVSVKVTYFDERIEIDALLTSQPHSPICSGCRPVRYOVLDPBPASGLPVVVTSH 840
| | | | |
Db 608 DGRVSVKVTYFDERIEIDALLTSQPHSPICSGCRPVRYOVLDPBPASGLPVVVTSH 667
QY 841 RKFLDVVTGCOMYOYVLAAGELGASPLNHNHGAAPVCGGKXSERLGECCDDGL 900
| | | | |
Db 668 RKFLDVVTGCOMYOYVLAAGELGASPLNHNHGAAPVCGGKXSERLGECCDDGL 727
QY 901 VSGGSCSKVCELEBGFNCVGBPSLCYMEBGDICEPERKTSIVDCGIYTPKGLDQWAT 960
| | | | |
Db 728 VSGGSCSKVCELEBGFNCVGBPSLCYMEBGDICEPERKTSIVDCGIYTPKGLDQWAT 787
QY 961 RAYSHEDKXKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMPCVASENETQDDREBP 1020
| | | | |
Db 788 RAYSHEDKXKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMPCVASENETQDDREBP 847
QY 1021 EGSILKKEDEWMLKXCFNRPGBARAIFLFTDGLVPGHQOPTYVTLVTVDRGSHSLGT 1080
| | | | |
Db 848 EGSILKKEDEWMLKXCFNRPGBARAIFLFTDGLVPGHQOPTYVTLVTVDRGSHSLGT 907
QY 1081 YGLSCOHNPILITNTHHONVLFHHTTSVLTNFSPPVGISAVALTSSRIGLSAPNSCIS 1140
| | | | |
Db 908 YGLSCOHNPILITNTHHONVLFHHTTSVLTNFSPPVGISAVALTSSRIGLSAPNSCIS 967
QY 1141 EDEGQNHQSGCIRPCGKODSCPSLLDHDVNVCTSIGGLMKCAITTCQGFALQASS 1200
| | | | |
Db 968 EDEGQNHQSGCIRPCGKODSCPSLLDHDVNVCTSIGGLMKCAITTCQGFALQASS 1027
QY 1201 GQYIRPMQKELLTLCSSGHMDQNSCLPYDCGVDPBSLVNANFSCSEGTFLKRCISIC 1260
| | | | |
Db 1028 GQYIRPMQKELLTLCSSGHMDQNSCLPYDCGVDPBSLVNANFSCSEGTFLKRCISIC 1087
QY 1261 VPPAKLQGLSPWLTCLBEDGLMSLPEVYCKLECDAPPIIINANLILPHCLQDNHVGITCK 1320
| | | | |
Db 1088 VPPAKLQGLSPWLTCLBEDGLMSLPEVYCKLECDAPPIIINANLILPHCLQDNHVGITCK 1147
QY 1321 YECKRQYVVAESABGKVRNKLKIQCLEGGIMEQSCIPVCEBPPPVFBGMEYCTNGFS 1380
| | | | |
Db 1148 YECKRQYVVAESABGKVRNKLKIQCLEGGIMEQSCIPVCEBPPPVFBGMEYCTNGFS 1207
QY 1381 LDSQCVANCNOERKLPILCTKEGLMTQEPFLCENLQGECPPPSELSNVEYKCEQGYI 1440
| | | | |
Db 1208 LDSQCVANCNOERKLPILCTKEGLMTQEPFLCENLQGECPPPSELSNVEYKCEQGYI 1267
QY 1441 GAVCSPCLVLPSPDPVWLPEINITADLTLEHMMEPVKQSIYCTGRQHPDPVLVHCIOQC 1500
| | | | |
Db 1268 GAVCSPCLVLPSPDPVWLPEINITADLTLEHMMEPVKQSIYCTGRQHPDPVLVHCIOQC 1327
QY 1501 EPPQADMCCTINNRAVCHYDGDCCSSTLSKKVIFPAADCDLDECTCRPKAENQ 1558
| | | | |
Db 1328 EPPQADMCCTINNRAVCHYDGDCCSSTLSKKVIFPAADCDLDECTCRPKAENQ 1385

RESULT 4
US-09-949-016-9436
; Sequence 9436, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949, 016
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
```

```
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 9436
; LENGTH: 717
; TYPE: PR
; ORGANISM: Human
US-09-949-016-9436

Query Match      19.8%; Score 1709; DB 4; Length 717;
Best Local Similarity 43.0%; Pred.No.5,1e-140;
Matches 310; Conservative 140; Mismatches 237; Indels 34; Gaps 14;

QY 851 GOMYQVLAAGELGASPLNHNHGAAPVCGGKXSERLGECCDDGLVSGGSCSKVC 910
| | | | |
Db 6 GSVYQVLAAGELGASPLNHNHGAAPVCGGKXSERLGECCDDGLVSGGSCSKVC 65
QY 911 ELEBGFNCVGBPSLCYMEBGDICEPERKTSIVDCGIYTPKGLDQWATRAYSHEDK 970
| | | | |
Db 66 RQVSVFNCIDEPSCYFHQDGVCEBEOKTSIKDCGVYTPQGFLOMASNASVSHD-Q 124
QY 971 KCPVSLVTGER-HSLICTSYHBDLPNHRPLTGMPCVASENETQDDREBPBGLKKEDE 1029
| | | | |
Db 125 QCPGWVILGQPAISOYCRKTVIDLSEGISQHAMVPCITISYPSYQ-----LAQTT 173
QY 1030 VMLKVCENRPGBARAIFLFTDGLVPGHQOPTYVTLVTVDRGSHSLGTGSCOHNP 1089
| | | | |
Db 174 VMLKVCENRPGBARAIFLFTDGLVPGHQOPTYVTLVTVDRGSHSLGTGSCOHNP 223
QY 1090 LITNTHHONVLFHHTTSVLTNFSPPVGISAVALTSSRIGLSAPNSCISEDEGQNHQ 1149
| | | | |
Db 234 LITNTHHONVLFHHTTSVLTNFSPPVGISAVALTSSRIGLSAPNSCISEDEGQNHQ 292
QY 1150 QSCIRHPCGKODSCPSLLDHDVNVCTSIGGLMKCAITTCQGFALQASSGQYIR 1205
| | | | |
Db 293 QSCIRHPCGKODSCPSLLDHDVNVCTSIGGLMKCAITTCQGFALQASSGQYIR 347
QY 1206 PMQ--KEILLTSSGHMDQNSCLPYDCGVDPBSLVNANFSCSEGTFLKRCISICVPP 1263
| | | | |
Db 348 PMQ--KEILLTSSGHMDQNSCLPYDCGVDPBSLVNANFSCSEGTFLKRCISICVPP 407
QY 1264 AKLQGLSPWLTCLBEDGLMSLPEVYCKLECDAPPIIINANLILPHCLQDNHVGITCK 1323
| | | | |
Db 408 AKLQGLSPWLTCLBEDGLMSLPEVYCKLECDAPPIIINANLILPHCLQDNHVGITCK 467
QY 1324 KPGYVVAESABGKVRNKLKIQCLEGGIMEQSCIPVCEBPPPVFBGMEYCTNGFS 1383
| | | | |
Db 468 KPGYVVAESABGKVRNKLKIQCLEGGIMEQSCIPVCEBPPPVFBGMEYCTNGFS 526
QY 1384 QCVLNC-----NOREKRLPILCTKEGLMTQEPFLCENLQGECPPPSELSN-VEYKCEQ 1437
| | | | |
Db 527 QCVLNC-----NOREKRLPILCTKEGLMTQEPFLCENLQGECPPPSELSN-VEYKCEQ 585
QY 1438 YGIGAVCSPCLVLPSPDPVWLPEINITADLTLEHMMEPVKQSIYCTGRQHPDPVLVHC 1497
| | | | |
Db 586 YGIGAVCSPCLVLPSPDPVWLPEINITADLTLEHMMEPVKQSIYCTGRQHPDPVLVHC 645
QY 1498 QSCPEPQADMCCTINNRAVCHYDGDCCSSTLSKKVIFPAADCDL-ECTCRPKAEE 1556
| | | | |
Db 646 QSCPEPQADMCCTINNRAVCHYDGDCCSSTLSKKVIFPAADCDL-ECTCRPKAEE 705
QY 1557 N 1557
| | | | |
Db 706 H 706

RESULT 5
US-09-911-842A-4
; Sequence 4, Application US/09911842A
; Patent No. 6656707
; GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
```

```

FILE REFERENCE: 01017/37592
CURRENT APPLICATION NUMBER: US/09/911,842A
CURRENT FILING DATE: 2001-07-24
PRIOR APPLICATION NUMBER: US 60/222,438
PRIOR FILING DATE: 2000-08-01
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PatentIn version 3.0
SEQ ID NO 4
LENGTH: 3594
TYPE: PRT
ORGANISM: Mus musculus
FEATURE:
NAME/KEY: misc feature
LOCATION: (1757)
OTHER INFORMATION: Xaa = any or unknown amino acid
US-09-911-842A-4

Query Match      3.9%; Score 336.5; DB 4; Length 3594;
Best Local Similarity 19.2%; Pred. No. 6,4e-19;
Matches 343; Conservative 189; Mismatches 626; Indels 629; Gaps 99;

QY 53 AFIVEAVKKEGGONNPAILAGVF---DNCSTVSDKMGALGIRSGKKGKRDARFFFS 108
DB 1476 AVTCAFMKSSDVINGPISYALEDDKDNFTLTDYNGWLVY-NGKEX----- 1524
QY 109 LCTDRVKKATLILSHKYPGTWTHVAATYD--GRHMAIYD-----GTQVASSLDQ 158
DB 1525 -----ITNCPSVNDIMHIAITWTISIGAMRVYIDGSLDGTSLSTGKAIPIG 1573
QY 159 SGPLNSPFMAKRSLLGSDSESDGHYFR-----GHILGLVFWSTAL-POSHFOSSQH 211
DB 1574 GG-----ALVIGQEDKKGEGFNPAESFVGSLSQNLMDYLSPOQVLLAS-- 1620
QY 212 SSGEAEATDLVLTAFFPVNTWVPFRDEKYPRLV-----LOGFEPEPILS 259
DB 1621 SCPEELSRGNVLA-----WPDFLSGITGKVKVSSWFCSDPSLEGSVPLHAPAS 1671
QY 260 PLQRPPLCGQYV---CD-NVELIS---QY---NGTW---PLRGEKIRYQVANNICDEGLNP 307
DB 1672 GNRKP--GSKVSLPCDGFQVGNPNVQYCLNQGQMTPLPFCERIR-----C--GLPP 1720
QY 308 IV-----SEBOIRLOHEALNEAFSRY-----NISMQSVHQNSTLRHRVYL 350
DB 1721 ALENGFISABDFRAGSTVYTOCTSGYLLGDSRPFCKDNGSN----- 1763
QY 351 VNCEPSKIGNDHCDPECEHPLTGYDGDCLQGRCYSMNRDGLCHVECNMLNDFDGD 410
DB 1764 -GISPSCLVDDECAV-----GSDCSEHASCMTN---GSYVCSNRPYTG-DGKN 1808
QY 411 CCDOVADVRKTCFDPDSPKRAYSVKELKALQNLSTHFLNIFYPASSVREDLAGAA-- 467
DB 1809 CAEP-----VKCAKAPENPEGRSS---GBIYTVGTA---VTFSCDEGHVGVSTIT 1854
QY 468 ---TWPKD-----DAYTHLGGIYLSRAYYGMGHTMTMHEGVHVLGLYHFGVS-- 516
DB 1855 CLETGEWDRLRPSCEALS--CGVPPVBNGVDSASFTYGSKV-----VTRCDGYTLTG 1907
QY 517 -ERESCNDPCKETVPSMETGDLCAATAPTPKSELCREPEPTS---TCGFTRRPGAFPT 571
DB 1908 DEESAC-----LASGS-WGSHSPVCGLVKCSQPEDINNKYLLSGLT----- 1948
QY 572 NYSYTDNCTNDNTNPQVARMHCYLDLVQQTBSKPTPIPIPEWVIGQ--TNKSLTI 629
DB 1949 -YLSIASYSCENGSLQGPSLLECTAGSGMDRAPSCQVLSGCBPPIVKAIVIGSPTF 2007
QY 630 HMLPPIGVVYDRAKSLGCACTEDGTFRQVYHTASSRNVCDSSGYWTPPE--AVG-- 683
DB 2008 -----GNIVATYCKEG-----YTLAGPDTIICQANGKMSNRHQLAVSCD 2048
QY 684 -PPVDQPCPSLQAMSPVHLVHMNTVPCPTGCSLELLFOHPVOADTLTLWVTSFPM 742
DB 2049 EPPVVDHA-----SPET-----ARLRGDT-----APYYC 2073

```

```

QY 743 ESSQVLFDTBELLENKESVHLGP-----LDTFCDIPLTIKLHVQKVGKVV----- 789
DB 2074 ADGYSLADNSQLICNAQGNVPPRGAQVPRCIAHFCEKPPSVSILSEYSKAFPAAGSV 2133
QY 790 -----YTFDERIEIDALLTSQPHSPICSGRPVRYOVLARDP-FASGLP----- 833
DB 2134 VSPKMGFVLNTSAKIECLRGSEWSPSLVQCIPIVR---CGRPPIANGVPSGTNVSF 2190
QY 834 --VVVTHSHRKFTDVEVTPGOMY---QYVLAERAGSELGEASPLPLNHI--HGAPYCGDGK 886
DB 2191 GAVVAVSGCHKGF-----YKGEKSTCEATQGMXKPTPCHPVSCEBPPVENG 2240
QY 887 VSERLGE-----ECDDGDVLVSGD-----GSKK----- 908
DB 2241 LEHTTGTTFSEBARFQCNPGYKAGSFVVCQANRHHSDAPLSTPLNCSKPPPIONGF 2300
QY 909 -----VCELEBGFNCVGPSPSLCYMYEGDICEPFRKTSIVDCGIYTPKGY 954
DB 2301 LKGSFPEVSGKVQVVC--NEGVELVDGNSMTQSGKMSKKR---SPKCVPTKCAEPRL 2355
QY 955 LDQWATRAYSHEDKKKCPVSLVT--GEPSLICSTYHPDLPHNRPLTGMP-----C 1005
DB 2356 ENQVLVKELEASE-----VGWMTISCKEGHALQPSVLKCLPESGQ--WNGSFPICKWVLC 2407
QY 1006 VASENETQDDRSBEQSGSLKKEDEVMLKVCNPRGEARLFI-----FLTTDGLVPSHQ 1060
DB 2408 -----PSRPL-----IPGVASSGALHFGSTVKYLCYDGF--LRG 2442
QY 1061 QPTVLYLTVDRGSNHSIGTYSQONPLIIN-VTHQNVLPNHTTSVLNFSPPVGI 1119
DB 2443 SPTI-LQADSTWSSPLPECVPVPCQPEELINQIINVQGLAVYLTLLYTKPPELVG- 2500
QY 1120 SAVAL--RTSSRIG--LSAPNSCISEDEGONHO-----GO----- 1150
DB 2501 NATTLGECNGQWLGKGMCKPIECREKELINGQFSSVFOYGQITIFYCDRGRLESPK 2560
QY 1151 -SCIHRPCKKQSCPSLLLDHADVNCSTIGP---GLMKCA-----ITGORGAL 1196
DB 2561 SLTCLF--TGWMDMP--PSCDAHCSDBQPLENGFVSGADYRYGAMITISCPRGQV 2614
QY 1197 QASSGQYIRPMQKEILLTCSSGHW--DONVCLPYDCGVP----- 1235
DB 2615 LGHAMQ-----TCRESGSSSSPTCVPRIDCLPHIIDGDCITKVRDGGHPDQ 2663
QY 1236 -----PSLVYANFSCSEGTGFL--KRCSTSCVPRAKLOGLSPWLT 1274
DB 2664 DDMMEVPEYLAHPQHLBATATAKALENTKESPAHASHFLYGTWVSYSCEPVELLGI-PLVLI 2722
QY 1275 CLEDEGLMSLEBYVC-KLECDAPRIILANILLPRCLDNHDVGTICKEGCPGYVAESA 1333
DB 2723 COEDGTWNGTAPSCISIECDLPVAPENGFL--HFTQTT--MGSAAQYSCRPGLHIBSH 2777
QY 1334 EGKVRNKLTIQICLEGIGWEGS--CIPVCEBPVPEGS-----MYECTN 1377
DB 2778 -----LRI-CLONQW--SGTYRCEALISCSRPNLMNGSTIGDDYSLGVLYECS 2827
QY 1378 GFSIDSCVLNCOERREKLPILCTKEGLWTOEFLCENLOGECPPPSBLN----- 1428
DB 2828 GYILNGSKKRTCOENRD-----WDGHEBWC--IPVDCSGPVPPTGRVKGSEYT 2874
QY 1429 ---SVEYKCGQY-----GIGAVCGRL-CVIRPSPVWMLREVITADTL 1467
DB 2875 FQKEITYSCEGFLLEGARBRICLTNGSWGATPSCNPRAPRQVY--NGVADGL 2929
QY 1468 E-----HMMEPVAVQS---IVCTGRQWHPDPLVHICQSCBP 1502
DB 2930 DYGFKEVAFHCEGYVLQGARPLTQGSNGTWDAE-----VPRCKP 2970

RESULT 6
US-09-911-842A-2
; Sequence 2, Application US/09911842A
; Patent No. 6656707

```

GENERAL INFORMATION:
; APPLICANT: Amgen Inc.
; TITLE OF INVENTION: C3B/C4B COMPLEMENT RECEPTOR-LIKE MOLECULES AND USES THEREOF
; FILE REFERENCE: 01017/37592
; CURRENT APPLICATION NUMBER: US/09/911, 842A
; PRIOR FILING DATE: 2001-07-24
; PRIOR APPLICATION NUMBER: US 60/222,438
; PRIOR FILING DATE: 2000-08-01
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO: 2
; LENGTH: 3571
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-911-842A-2

Query Match 3.88; Score 330.5; DB 4; Length 3571;
Best Local Similarity 19.9%; Pred. No. 2,1e-18;
Matches 353; Conservative 207; Mismatches 612; Indels 603; Gaps 106;

53 AFTVEAVVKEGQGNPAIIAGVFDNCSHT---VSD-KGMALGIRSGKDKGRARFFFS 108
Db ALITTFPMKSSDDNNYGTPTISYAVDNGSDNTLLITDNGWLVY-NGERK----- 1498
Qy 109 LCTDRVKKATILISHSRYPGTWTHVATYDGRH--MALYVDGTQVASSLDQSGPLNSPF 166
Db -----ITNCPVNDGRMHIAITWTSANGIMKVIYIDGKLSGGAGLSVGLIIP- 1546
Qy 167 MASCRSILLGDSSEDEGHYR-----GHIGTIVFWSTAL-POSHFGHSSQHSQSGEEBAT 219
Db -----GGGAVLQGEODKKEGFEFASFEVGSISQLMLMIVLSPQ---QVKSILATSCPEELS 1601
Qy 220 DLVLTASFEPNVTWVPR-----DEK-----YPRU-----EVLQ----- 249
Db 1602 KGNVLA-----WPDLSGIVGKVKIKDSKIFCSDCPRLGSGVPHLRTASEDLKAGSK 1653
Qy 250 -----GF-----EBEP---EILSPLQPL-----CGQTV- 270
Db 1654 VNLFCDFGLVGNPVQYCLNQGMQTPRLPHCERISGCVPRPLNGFHSADDPYAGSTVT 1713
Qy 271 --CDNVELISQYNGYWPRLGKQIRYOVNICEDEGLNPIVSEQIRLQHEALNEAFSR 328
Db 1714 YQCN-----NGUYLLGDSRM-----FCTDNGSMNGVSPCLVDDECAVSGDSEH 1758
Qy 329 NISMQLSVHQHNSLTLRHVLVNCEPSKIGN-DHC-DP--BCE---HPLNGDGGDLQ 382
Db 1759 ----ASCCLNDVGS-----YTCSGCVPRYTGDGNCAPIKCKAPENSHSGELIYTV 1807
Qy 383 G-----RCYSWNRDGLCHVE-----NMMLANDPDGDCDDPOVADVRKTCFDPDSPKR 431
Db 1808 GAEVTFSCQEGYQLMGVTKITCLESSENMHLI-----PYCKAV--SCGKPAIPEN 1855
Qy 432 AYNSVKELKALQLNSTHFLNITFASVREDLAGAATWPMDKAVTHLGGIVLSPAYYM 491
Db 1856 G-CIEELAFTFSGKVIYRCMKGYTLAGDKXESSCLANSSWSHSPR-----VCEPRVCCSS 1907
Qy 492 PGHDTMIMHEGNGHLYGHVFKGVSEKSCNDPCKETVPSWETDLCADTA-----P 543
Db 1908 PENINN-----GKT-IISGLTYLSTASYC-DTGYLSQGSIIECTASIGMDARP 1956
Qy 544 TPKSELCREPEPSTDC-----GFTRFPGAPFTNMTSYTDNCTDNFTPNQVAMHCYIDL 599
Db 1957 ACHLVFGGEPRAIKDAVITGNFT-----FRNTVTYT--CKRGYTLAGIDTIECLAD- 2006
Qy 600 VYQQWTSRK--FTPIPIPMVIGQTNKSLTIHMLPRLISGVVYDRASGSLCGATEDGT 656
Db 2007 --GKMSRSDDQCLAVSCDEPPIVDHASPE--TAH-----RLFGLIAFYCYSDG- 2050
Qy 657 FROVYVHTASSRRVCDSSGYWPREAVGPRD--VDPRCE--PSLOAMSPBVHLIYHNMNTVPC 713
Db 2051 ---SILADNSQLCLNAGQKWPBPGQMPRCTIAHFCEKPPSVS-----YST----- 2093
Qy 714 PTBEGSLELLFOHPVQADTLTLMTWTSFFMESSQVLPFTLEILLE-----NKESVHLGPL 766

Db 2094 -----LESYSKAKFAAGS-----VSPFKMEGFVL-NTSAKICBMGGQGNPSPMSIQCI 2142
Qy 767 DTFCDDIPLTIKLAVDQKSVGVKTYTDERI-----EIDAALLTSQPHSLCS 813
Db 2143 PVRCGEPPSI---MNGVAGSN--YSFGAMVAVSCNKGFIYKGEKSTCEATGQWSSFTPT 2198
Qy 814 GCRPVRYQVLRDPPFASGLPVVVTTHSHRKFTDVEVTPGQWYQYQVLAAGELGEASPL 873
Db 2199 -CHPV-----SGGEPKVENGR-----LEHTTGRIFSEBVRQCPGYKSVSPV 2242
Qy 874 -----NHIG-APY-----CG-----DGKYSRLGECDDGLVSGDGS 907
Db 2243 FVCOANRHHMSESPLMCPVPLDCGKPPRIQNGFMKGFENFVSGKVQFCNCGEYLVDGS-S 2301
Qy 908 KQCELEBGFVQVCEPRLCYVYEDGICEPE-----RKTSIVCGIYT--PK 952
Db 2302 WTCQKSGKMKKSNPK-----CMPEKCEPRLLENQVLVKELTTEVGVVTFSSCKE 2351
Qy 953 GYL-----DOMATRAYSHEDKKKCVSLVTEGPHSLICTSYHPLDN--HR 997
Db 2352 GHVLOQPSVLKCLPSQW-----NDSPPVCKIVLCTPP--LISFVPIPSALHF 2400
Qy 998 PLTGMPPCVAS-----ENETQDDRSQEPQSGSLKKEDEVW--LKVCENRPEBAIIFLIT 1050
Db 2401 GSTVYKSCVGFPLRGNST-----TLQPDGTWSSPLPBC----- 2435
Qy 1051 TDGLVPRGHQOP--TVTLTYLTVRQSGNSHSLGTGLSQOHN--PLIINV--HHQNVLFH 1104
Db 2436 ---VPECPQPEIPINGIITDVOGLAV--LSTALYTCPEGLVGNVTTLLCGENHMLGK 2490
Qy 1105 TTSVLNFSPPRGVSAVALRTSRLGSAFNSCISEDEGQNHQGS---CIRHPCGKOD 1161
Db 2491 PTCKAIECLKPKRIINGKSFYTDLHGQVITYSC---NRFRLGEGSALICL--TQDWD 2545
Qy 1162 -SCPSSLIDHADVNCSTIGP--GLMKCA-----ITCORGRALQSSQYIRPMQ 1208
Db 2546 VDAPS-----CNAIHCDSPQPIENGFEAGADYSYGAIIIVSCPPGVOAGHAMQ----- 2594
Qy 1209 KEILITCGSSGHMQUV--SCLPVUDGVP-----DPSLVNY----- 1241
Db 2595 -----TCESGWSSTSPICMPIDCGLPRIIDFGDCTKLKDDQGYFEOEDMMBEVPTVTPH 2649
Qy 1242 -----ANFSCSEGTK-----FL--KRCSISCVPAKQGLSPWLTCLEGLMSLP 1284
Db 2650 PPHYHGAIVAKTMENTESPAHTSSNFLXGTMVSYTCNPGVELLG--NPVLLCOGDGTWNGS 2708
Qy 1285 EYVC-KLECDAPRIILNANILLPHCLQDNHDVGTICKYECKPGYVVAESAEGVNRKMLK 1343
Db 2709 APSCISIECDLPTAPENGFLRFTET-----SMGSAVOQSCPKGHILVGSQ-----LR 2755
Qy 1344 IQCLEGSIWQGS--CIPVYCEBPVPVFBG-----MYECTNGFSLDSQCVLN 1388
Db 2756 L-CLENKNSGASPRCAISCKKRNPMNGSIYGSNTYIISTLYEBCDPGY-----VLN 2808
Qy 1389 CNOERKLPITCTKEGLITQEFLLCENLOGECPRPSEILN-----SVEYKCEQ 1436
Db 2809 GTERR-----TCDDKNWDEBEPIC--IPVDGSPVSNAGQVRGDEYTGKEIEYTCNE 2861
Qy 1437 GY-----GIGAVCSPL--CVIRPSPDWMLPENITADTLEHNMERYK-- 1475
Db 2862 GFLLEGARSFVCLANGSWSGATPDCAVVRCATPR-----QLANGVTBLDYGFMKELVTFHC 2917
Qy 1476 -----VQSIYCTGRQCHNRPVLVHNCQSEPR 1502
Db 2918 HEGYIILHGAARKLTCQSDGNDAE-----IPLCKP 2946

RESULT 7
5256642-10
; Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.; KLUICKSTEIN, LLOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN

```

;H, MAKRIDES, SAVVAS, MARSH, HENRY C. JR.
; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
; RECEPTOR 1 (CRI) AND A THROMBOTIC AGENT, AND THE METHODS OF
; USE THEREOF
;
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,128
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1988
; SEQ ID NO:10:
; LENGTH: 1847
;
Query Match      3.3%; Score 287.5; DB 6; Length 1847;
Best Local Similarity 19.1%; Pred. No. 4.1e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

QY 221 LVLTASPEPVNT-EMVPE-----RDE-----KYPLEVLQGEPEPEPILSPLOPL-- 265
DB 39 LALPVMAGCCNAPEMLPFAAPNTLDEPEPPIGTYLMECPKPGYSGRPFSTICLKNSVMT 98
QY 266 ----CGQTVCDN-----VETLSQNGYWPRLRGEKI 292
DB 99 GAKDRCKRKSQBNPDPVNGVNVHVKIGIQGSOIKYKCTGKYLIGSSATCIIISGDTVI 158
QY 293 RYQVNICD--DEGLNIVSEBQIRLOHEALNEAF--SRYNISWQLSVHOVHNSTLRHR 347
DB 159 WDNETPLCDRIPCGLPPTIT-----NGDFISTNRENFHY-----GS 194
QY 348 VLVNCEPSKIGND-----HCDPECEPLTYGDG--DCRLQRCYSNRRDGL 394
DB 195 VVYTRCKPSSGGKRVFELVGEPSITYCTSNDDQ--VGWSGPAPOCIIIPNKCTPPNVZNGI 252
QY 395 CHVECNMM--LNDPDDDC--C-----DPOVADVKTCEPDSPKRAY 433
DB 253 LVSDNRLSFLSNEVVERCPQVFVMKGPBRVYKCOLNKMWELPSCGRVCOQPPDVLHA- 311
QY 434 MSYKELKEALQILNSTH--LNTYFASVREDLAGAATW-----PMDKDAVT----- 477
DB 312 -----ERTORDKNFSPGOEVYFVSCPEGYDLGASMSRCTPOGDSWSPAPTCVXSCD 364
QY 478 ----HLGGIVLSPAYYGMGHTDTMHEVGHVLG--LVHVPKG-----VSERE 519
DB 365 DFNGQLNGRVLFPVNLQIAKVDVFCDEGFOGLKSSASVYCVLAGMESLNNSVVPEQI 424
QY 520 SCNDPCKEIVPS-METG-----DLCAD----- 540
DB 425 FC--PSPPVLPNGHHTKPLEVFPFGKAVNYTCDPHNDRGTSFLLIESTIRCTSDQGN 482
QY 541 ----TAPPKSEL--CREPE-----FTSDTCGTRPP--GABFTNYS 575
DB 483 GWSSPAPRCGILGHCOAPHFPLPAKLKTOTNASDFIGTSLKECEKPEYVGRFSS---- 538
QY 576 YTDNCTCNF--TPNGVAMHCVLDLVQOMTESRKPPIPIRPVW----- 619
DB 539 ----ITCLDNLVWSSPKVVC-----RKSKCTPPDVMGMVHVTIDIOVGSRIIN 583
QY 620 ----IGQTNKSLTI-----HW--LRPI-----SGVVYDASGSLGACTEDGTFR 658
DB 584 YSCGTGHRILGHSAECISLGNANAWSTKPIICORIGLPRTIANDPI-----STNR 637
QY 659 QYVHTAS--SRVVDSSGYMTPEAVGPRDV-----DQCEBRLQAMS--PEVHLVMMN 709
DB 638 ENFHYGVVYVYRCNPGSGKRVFELVGEPSITYCTSNDDQ-----VGWSGAPPOCIIIPNK 692
QY 710 TVPCPTGSGLELLFGPRVQADTLTLMTVTSFFMESOVLPFTTEILLE--NKESVHLGPL 766

```

```

DB 693 CTPPNVE-----NGILVSDNRLSFLSNEVVERFCQPGFVMKGP 731
QY 767 DTGCDPIPLTIKLAVDKVSGVKYTFPDERIEIDALLTSOPHPLSGG--CRPARVQVLRD 825
DB 732 RVKCO-----ALNKMPEBELPSCGRVCOQ----- 754
QY 826 PPFASGLPVVYVTHSHRKFTDVE--VTPGQWYQVULAEAGEL--GEAS-----PLNHTHGA 879
DB 755 ----PPOVLAERKQDKDNFSPQEVFTS--CEPGYDLKGAASMRCTPOGDSWSPAA 805
QY 880 PYCG-----DGK--VSERLGEE--CDQDGLVSGDGS----- 907
DB 806 PTCBVYSCDDFMQGLNGRVLFPVNLQIAKVDVFCDEGFOGLKSSASVYCVLAGMESLNN 865
QY 908 --KVCE-----LE-----EGRNCVGEPSL-C 925
DB 866 SSVPVCEQIFCPSPPVLPNGRHTGKPLEVFPFGKAVNYTCDPHNDRGTSFLLIGESTIRC 925
QY 926 YM-YEGDGI-----CE-----PPEKTSIVDCGIYV-----PKGY-- 954
DB 926 TSDPQNGVWSSPAPRCGILGHCOAPHFPLPAKLKTOTNASDFIGTSLKECEKPEYIGR 985
QY 955 ----LDQWATRAYSSHED--KKKC--FVSLVTGSPHSLI-----CTSYHND 992
DB 986 PFTITCLD--NLVWSSPKVCKRKSCKTPDPVNGVNVHVTIDIOVGSRIINYSCTTGH-R 1041
QY 993 LPNHR-----PLTGMFPC--VASENETODDRSEQBPGLKKEDEV 1030
DB 1042 LIGHSAAECILSGTAMHSTKPIQRIPCGLPPTIANGDFISTNRENFHYGSV----- 1095
QY 1031 WLKVCNFRPEBAALF-----IFLTIDG-----LVPEBHQOPIYT--LYL 1068
DB 1096 -VYTRCKLSSGRKRVFELVGEPSITYCTSNDDQVIGWSGPAPOCIIIPNKCTPPNVZNGI 1154
QY 1069 TDVRGSNHSI-----GTGLSGCQ-----HNPLIINYTHHQNVLFI 1103
DB 1155 SD-----NRSILFSLNEVVDPRCQPFVMKGPBRVYKCOLNKMWELPSCGRVCOQPPDVLH 1210
QY 1104 --HTTSVLLNFPSSPRNGISAVALRTSRIQLSAPNSCISDEGQNHOGQCTIHRPCGQ- 1160
DB 1211 GEHTPSHODNFSF-----GOEVYFSC--EPGYDLGASLSH--CTPPOG 1249
QY 1161 ----DSCPSLL--LDHADVYVNTSIGGLMKCAITOCRGFALQASSGQYIRPM 1207
DB 1250 DWSPEARCAVYKSCDDDFGLQPLPHGRVLPPLNLQIG-AKVSFVCDGFRLLKSSVSH---- 1304
QY 1208 QKEIILLTSSGHWQDQVNS--CLPYDCGVDPDSLNVYANFSCSEG--TKFLKXCSISCV- 1262
DB 1305 ---CVLVGMSLNNNSVPUVCEHIFCPNP--PAILNGRHTGTPSGDIPYKXESTYCDHPD 1360
QY 1263 ---PAKLOGLSPLWLTLED--GLWSLPEVYCKL-----ECDAPPIILNANILLPHCLO 1310
DB 1361 RGMTFNLIGEST--IRCTSDPHGNGVWSSPAPRCBELSVRAGHCKTPGFPFASPTIP--IN 1417
QY 1311 D-NHDVGTICKYCKPBYUYAESAEGVKNKLLKIQCLEGGIHE--QGSCLPVVCEPRP 1367
DB 1418 DFEPPVGTSLNYCECRPGYF-----GKMFSISCLLENLWSSVSDNCRRRKSSCGPRPE 1467
QY 1368 VFEQGM-----YECTNGFSL--DSQCVLNCQBEREKLPIILCTKEGLWTOE 1409
DB 1468 PFNGMWHINIDTQFGSVVYVNSCBNGFRLLISPTTCLVSGNNV-----TWDKK 1515
QY 1410 FKLCEMLQGECPPEPSELNS-----VEYKCEQGYG----- 1439
DB 1516 APICEIT--SCBPPPTISNDGDFYSNNRTSPHNGTIVVYVYQCHGTGPDGQLFELVGERSIYC 1573
QY 1440 ----IGAVCSP-----LCVIIP--SDPVWLPEBIT--ADTLEHMMER--VKV 1476
DB 1574 TSKDDQVGVWSSPPRCISTNKTAPAEVENAIRVGNRSFSLTEIRFCQPGFVWGS 1633
QY 1477 QSIIVCTGRQWHPDPVLVHCIOGCEP 1502
DB 1634 HTVQCCQTNGRW--GPKLPHCSRVCOQ 1657

```



```

Qy 1440 -----IGAVSP-----LCVIPP-SDPVMLPENT-----ADTLEHMEP-----VKV 1476
Db 1574 TSKDQGVWSSPPRCISTNKCTAPBEVNAIRVGNRSFSLTEIIRFCQPGFVWGS 1633
Qy 1477 OSIIVTGRWHPDVLVHCIOGCEP 1502
Db 1634 HTVOCQNGRW--GPKLPKCSRVCP 1657

RESULT 9
5256642-10
Patent No. 5256642
APPLICANT: PEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (C1) AND A THROMBOTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1986
SEQ ID NO:10
LENGTH: 1847
5256642-10

Query Match 3.3%; Score 287.5; DB 6; Length 1847;
Best Local Similarity 19.1%; Pred. No. 4.1e-15;
Matches 349; Conservative 178; Mismatches 546; Indels 751; Gaps 105;

Qy 221 LVLTASEPVNT-EMVPP-----RD-----KYPRLVQLGEPPEBELSPLOPL-- 265
Db 39 LALVAVAGQCAPELPPARPTNLDEBEPIGYLYNECRGYSGRFSIICLKNSVMT 98
Qy 266 -----CGQTVCDN-----VELISQYNGWPLRGEVY 292
Db 99 GAKDRCRRKSKRNPDPVNGVNHVYKIQFGSQIKYCTKGRYRIGSSSATCIIISGDTVI 158
Qy 293 RYGVVNICD--DEGLNPIVSEQIRLOHEALNEAF--SRYNISMQLSVHQVHNSTLRHR 347
Db 159 WDNETPLCDRIPLGIPPTIT-----NGDPISITNRENFHY-----GS 194
Qy 348 VLVNCEBSKIGND-----HCDPECEHPPLTGYDG--DORLOGRCYSWNRDGL 394
Db 195 VVTVRCNPGSGRAKVFELVGEPSIYCTSNDDQ--VGWISGAPACIIIPNKCTPPNVEGKI 252
Qy 395 CHVCANNM--LNDPDDGDC-----C-----DPQVADVKTCTDPSPRAY 433
Db 253 LVSNDNRSLFSLNEVVEFCQPVFMKGRARVCOALNKMEBELPSCSRVCPDPVLAHA- 311
Qy 434 MSVXELKALQLNSTHF--LNIYFASVREDLAGAATW-----PMDKXAVT----- 477
Db 312 -----ERTORDKNBSFGQEVFYSCPEGYDLNGAASMRCTPGQDMSPAAPTECVKSCD 364
Qy 478 -----HLGGIVLSPAYYGMPTDTMIHEGVHVLG--LYHVFPGK-----VSERE 519
Db 365 DFMGQLNLNGRVLFPVNIOLGAKVDFVCEGFLQKSSASYCVLAGMESLWSSVYVCEQI 424
Qy 520 SCNDPKCKETVS--METG-----DICAD----- 540
Db 425 FC--FSPPEIIPNGRHGKPLEVFPFGKAVNYTCDPHPDRGTSFLLIGSTIRCTSDPOGN 482
Qy 541 ---TAPFKSEL---CREEP-----FTSDTCGFTRP--GAPFTWMS 575
Db 483 GWSSPAPRCIGLHCQAFDHFPLAKLKTQTNASDFIGTSLKTECRPEYIGRFPSS----- 538

```

```

Qy 576 YTDNCTDNF---TPNOYAKMHCYLDLVQOQWTESKRPPIPIPPMV----- 619
Db 539 ---ITCLDNLVWSSPKVCK-----RKSKCTPPDPVNGVNHVITDIQVGRIN 583
Qy 620 -----IGQTKSLTI-----HW--LPPI-----SGVYDASGSLCACTEDGTFR 658
Db 584 YSCTGHRILGHSSAECLISGNAAMHSTKPPICORICGLPPTIANDFT-----STNR 637
Qy 659 QYVHTAS--SRRVCSGWTTPBEAVGPPDV-----DQCEPSLQAMS--PEVLYHNMN 709
Db 638 ENFHYGSVWTVYRCNPGSGRAKVFELVGEPSIYCTSNDDQ-----VGWISGAPACIIIPNK 692
Qy 710 TVPCPTGCCLELLFQHPVQADITLTMTSPFMESSQVLPDTLELL--NKEVHLGPL 766
Db 693 CTPEPNEV-----NGILVSDNLSFLNEVVEFCQPGFVWGP 731
Qy 767 DTPCDIPLTIKLHYDGKVGKVTTPDBRIEIDALLTSOPHSPLCSG--CRPVRYQVLRD 825
Db 732 RVKCO-----ALNKMEBELPSCSRVCP----- 754
Qy 826 PPFASGLPVVVTSHRKTDFVE--VTPQOMYQVLAAGEEL--GEAS---PPLNHTHGA 879
Db 755 -----PPVLAHERTQORDKNBSFGQEVFYSS--CEPGYDLRGAASMRCTPGQDMSPA 805
Qy 880 PYCG-----DGK--VSRUGEE--CDDGLVSGDGS----- 907
Db 806 PTCVKSQDDFMGQLNLNGRVLFPVNIOLGAKVDFVCEGFLQKSSASYCVLAGMESLWN 865
Qy 908 ---KVCE-----LE-----EGFNCVGEPSL-C 925
Db 866 GSVPVCEQIFCPSPPIVINGRHGKPLEVFPFGKAVNYTCDPHPDRGTSFLLIGESTIRC 925
Qy 926 YM-YEGDGI-----CE-----PPEKRTSYVDCGIYT-----PKGY-- 954
Db 926 TSDQNGWSSAPRRCIGLHCQAFDHFPLAKLKTQTNASDFIGTSLKTECRPEYIGR 985
Qy 955 -----LDQATRAYSHED--KKCC--PVSIVTGEPSHIL-----CTSYHPD 992
Db 986 PFSITCD---NLWSSPKVCKRKSCKTPDPVNGVNHVITDIQVGRINYSCTTGH-R 1041
Qy 993 LPMNR-----PLGWFPCC-----VASENETQDRBQPGSLKKEBEV 1030
Db 1042 LIGHSSAECLISGNTAMSTKPPICQRI PCGLPPTIANGDTSTNRENFHYGV----- 1095
Qy 1031 WLKVCFNRPGEARAIF-----IFLTDDG-----LVPSHQQPTV--LYL 1068
Db 1096 -VTVRCNLGSRGKRVFELVGEPSIYCTSNDDQVGWISGAPACIIIPNKCTPPNVEGKI 1154
Qy 1069 TDVRGSHSL-----GTYGLSQ-----HNPLIINYTHQNVLFH 1103
Db 1155 SD-----NRSFLSFLNEVDFPCQPGFVFMKGRARVCOALNKMEBELPSCSRVCPDPPEILH 1210
Qy 1104 ---HTTSVLNPPSSPRVGISAVALTSSRIGLSAASNCSISEDEGNGHGGSCGSIHRPCKQ- 1160
Db 1211 GEHTPSHQDNFSP-----GQEVFYSC--BPGYDLGASLH--CTPQG 1249
Qy 1161 -----DSCPSLL--LDHADVNCTSIGGLMKCAITCORGFALQASGQYIRPM 1207
Db 1250 DMSPEARCAVKSQDDDLGQLPHGRVLPPLNLOLG--AKSVFVCEGFLKSSVSH----- 1304
Qy 1208 QKEILLTCSGGHMDQVNS--CLPVDCGVDPDSLVANVANSFSGSEG--TKFLKRCISICVP-- 1262
Db 1305 ---CVLVGMRSLWMSVPCVEHIFCPNP--PAILNGRHGTGTPSGDI PYGKEISYTCDDPHD 1360
Qy 1263 ---PAKQGLSPMLTCLD---GLWSLPEVYCL-----ECDAPIILNANULLPBCLO 1310
Db 1361 RGMTFNLIGEST--IRCTSDPHGNGWSSAPRRCGLSVRAGHCKTPEGPPRASPTTP--IN 1417
Qy 1311 D-NHDVGTICKYECKPQYVVAESAEGKVRNKLKIQCLEGGIWE--GSGCIPIVVCBPP 1367
Db 1418 DFERPVGTSLNTEBERPOYF-----GKMPSISCLLENLVWSSVNDNCRKRSKCGRPP 1467

```

QY 1368 VEEGM-----YECTNGFSY-----DSQCVLNCQBEREKLPICTKEGLWTOE 1409
Db 1468 PFNGMWHINTDTQSGSTWYNSCNEGFRILGSPSTTCLVSGNNV-----TMDKK 1515
QY 1410 FKLCEINLOGECPPEPSEILNS-----VEYCKBOGYG----- 1439
Db 1516 APICEII--SCEPPTLISNGDFYNSNRTSFHNGTWTYQCHTGPDEQLFELVGERSIYC 1573
QY 1440 -----IGAVCSP-----LCVIRP-SDPVMLEPENT--ADTLEHMMEP-----YKV 1476
Db 1574 TSKDDQGVWSSPPRCISTNKKCTAPEVENAIRVGNRSFPLTEILIRFCQPGFVMVGS 1633
QY 1477 QSIIVCTGRQWHPDPVLVHCIOSCP 1502
Db 1634 HTVOCQNGRM--GPKLPHCSRVQCP 1657
RESULT 10
5472939-10
; Patent No. 5472939
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; JIP, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
; MEDIATED DISORDERS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138, 825
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588, 128
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 412, 745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332, 865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176, 532
; FILING DATE: 01-APR-1988
; SEQ ID NO: 10:
; LENGTH: 2006
5472939-10
Query Match 3.3%; Score 287.5; DB 6; Length 1847;
Best Local Similarity 19.1%; Pred. No. 4.1e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;
QY 221 LVTLASEEPVNT-EWVP-----RDE-----KYPLEVLQGEPEPEILSPVQPPV-- 265
Db 39 LALPVAMQOCNAPEWLPAPRPNTLDEFEPIGTLYNECRPGYSGRFSIICKNSVWT 98
QY 266 -----CGQTVCDN-----VELISQVNGVWPLRGEKVI 292
Db 99 GAKRCRKRKSCRNPDPVNGMWHVYIKGIQFSSQIKYCTKGRILIGSSATCIISGDIIV 158
QY 293 RYQVAVNICD--DEGLNPVSEEQIRLQHEALNEAF--SRYNISMQLSVHQNSTLRRH 347
Db 159 WDNRPICDRIPCGLPRTIT-----NGDPISITRENRFY-----GS 194
QY 348 VVLVNCBPSKIGND-----HCDECHPLTGDG--DCLQGRICYSMRRDGL 394
Db 195 VVTVRCNCGSGGRKVFELVGPBSIYCTSNDDQ--VGISGAPAPCIIIPNCKTPPVNENGI 252
QY 395 CHVECNMM--LNDPDDGC-----C-----DPOVADVKTCTDPSPKRAY 433
Db 253 LVSDNRSLFSLNEVVEFRQCPVFMKGRRYKCALNKWBEPLSCSKVCPDPDVLAHA 311
QY 434 MSVXELKEALQINSTHF--LNIYFASSVREDLAGAATW-----PMDKDAVT----- 477
Db 312 -----ERTQRDKDNFSPGQEVFVFSCEPGYDLRGAASMRCTPGQDWSPAAPCEVNSCD 364
QY 478 -----HLCGYLSPAYYMPGHTTMTHEVGHVUG--LYHVFNG-----VSERE 519
Db 365 DFMQQLNGRVLFPVNLQLAGKVDVFCDEGFOLKSSASCYVLGMESLMNSVAVPVEQOI 424

QY 520 SCNDPCKEIVPS-MENG-----DLCAD----- 540
Db 425 FC--PSPPVLPNGRHKPKLPEVPPFGKAVNYTCDPHRDGRTSDLDGESTIRCTSDPQGN 482
QY 541 ---TAPPKSEL--CREPE-----PTSDTCGFTRPP--GAPFTNYS 575
Db 483 GWMSSPAPRCGILIGHCOAPDHFPLFAKLKTQTNASDPPIGSLKYECRPEYGRFSS-- 538
QY 576 YTDNCTDNF--TPNOVAMHCYLDLVYQWESRKPPIPIRPVW----- 619
Db 539 ---ITCLDNLVWSSPKDVCK-----RKSCPTDPVNGMWHVITDIQVGRIN 583
QY 620 -----IGQTNKSLTI-----HW--LPPI-----SGVYDRASGSLCGACTEDGTFR 658
Db 584 YSCCTGHRILIGHSABECILISGNAAMHSTKPIQRIPCGLPRTIANGDPI-----STNR 637
QY 659 QYVHTAS--SRVCDSSGYWTPBEAVGPPDV-----DQCEPSLOAMS--PEVHLTHMM 709
Db 638 ENPHYGSVVTYRCNPGSGGRKVFELVGPBSIYCTSNDDQ-----VGISGAPAPCIIIPNK 692
QY 710 TVPCPTGCGLELIFQHPVQADTLTLMWTSFFWESSQVLPDTEILLE--NKESVHLGFL 766
Db 693 CTPEPNE-----NGILVSDNRSLFSLNEVVEFRQCPGFVMKGR 731
QY 767 DTFCDIPLTIKLHVDKVSQVYTFDERIEIDALLTSQPHSPILSG--CRPVRYOVLRD 825
Db 732 RVKCO-----ALNKKMEPLPSCSRVQCP----- 754
QY 826 PPSAGLPVVVYTHSRKRTDVE--VTPOQMYQYVLABAGSEL--GEAS--PLNHIHCA 879
Db 755 -----PPDVLAERTQRDKDNFSPGQEVFVS--CEPGYDLRGAASMRCTPGQDWSPA 805
QY 880 PYCG-----DGK-----VSRILGEE-----CDDGDLVSGDGS----- 907
Db 806 PTECVNSCDDFMQQLNGRVLFPVNLQLAGKVDVFCDEGFOLKSSASCYVLGMESLMN 865
QY 908 ---KVCE-----LE-----EGFNCGEBSPL-C 925
Db 866 SSVPVCEQIRCPSPVPIPNGRHNGKPLEVPPFGKAVNYTCDPHRDGRTSDLDGESTIR 925
QY 926 YM-YEGDGI-----CE-----PPEKRTSLVDCGIYT-----PKCY-- 954
Db 926 TSDPQGVWSSPAPRCGILIGHCOAPDHFPLFAKLKTQTNASDPPIGSLKYECRPEYGR 985
QY 955 -----LDQWATRAYSHED--KKKC--PVSLVTGEPHSLI-----CTSYHPD 992
Db 986 PFSITCLD--NLVWSSPKDVCKRKSCKTIPDPVNGMWHVITDIQVGRINYSCTTGH-R 1041
QY 993 LPNHR-----PLTGWFPD-----VASENETQDDBSEQBSLKKEDEV 1030
Db 1042 LIGHSSABECILISGNTAMHSTKPIQRIPCGLPRTIANGDPISTNENRPHYGSV----- 1095
QY 1031 WLKVCENRPEEAPAI--IFLITDG-----LVGEHQQPVYT--LYL 1068
Db 1096 -VTVRCNLGSRGRKVFELVGPBSIYCTSNDDQVGISGAPAPCIIIPNCKTPPVNENGI 1154
QY 1069 TDVRSNHSI-----GTYGSCQ-----HNPLIIVTTHQNVLFH 1103
Db 1155 SD-----NRSFLFSLNEVVDFFRCQPFVMKGRRYKCALNKWBEPLSCSKVCPDPDILH 1210
QY 1104 ---HTTSVLNFFSSPRAVISAVALRTSRIGLSAPNSCISDEBQOMHGOGSCIHPPCGQO- 1160
Db 1211 GEHTPSHODNFS-----QGEVYFSC--EPGYDLRGAASLH--CTPQG 1249
QY 1161 -----DSCPILL--LDHADVNTCSIGBLMKKAITCORGFALQASSQGIYRPM 1207
Db 1250 DMSPEAPRCAYKSCDDFLGQLPGRVLFPLNLDLG--AKVSFVDCBGRRLGSSVSH----- 1304
QY 1208 QKXELILTCSSGHHQDQNS--CLPVDGVPDPSLVANVNFSCSEG--TKFLKRCSTISCV- 1262
Db 1305 ---CVLWGRMSLMNNSVAVPVECHIFCPNP--PALINGRHTGPSGDIIYGEKISTYCDPHPD 1360

1263 ---PAKLOGLSPMLTCLD---GLMSLBEVYCKL---BCDAPILLNANLLPHCLQ 1310
1361 RGMFTNLIGEST-IRCTSDPHGNVWSSPAPRCESIVRAGHCKTPEQPPSPPTP-IN 1417
1311 D-NHVDGTICKECKPGYVYASAGKVRNKLKIQLEGGEWE--QSCSPVVCCEPPP 1367
1418 DFFPVVGSILVYECRPGYF-----GKMFISCIENLVMSVEINCRKSGCPPE 1467
1368 VFEGB-----YECTNGFSL---DSQVLINCQERKELPILCTKGLWTOE 1409
1468 PFNGVHINTDTORGSTVYVASCNEGFRLIGSPSTCLVSGNNV-----TWDXK 1515
1410 FKLGENLOGECPPESELS-----VEKCEQGYG----- 1439
1516 APICEII--SCPEPTISNGDFYSNNRTSFHNGVTVYQCHTGPDEQLFELVGERSTYC 1573
1440 ---IGAVCSP-----LCVIP--SDPMLPENIT---ADTLEHMMEP---YKV 1476
1574 TSXODQVGVWSSPPRCISTKCTAPBEVNAIRVGNNSPFSLEIIRFCQPGFVWGS 1633
1477 QSVICTGRQHPDPVLVHCIOQCEP 1502
1634 HTVOCOTNGRW--GPKLPHCSRVCP 1657

RESULT 11
5256642-2
Patent No. 5256642
APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IF, STEPHEN
H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
RECEPTOR 1 (CPL) AND A THROMBOLYTIC AGENT, AND THE METHODS OF
USE THEREOF
NUMBER OF SEQUENCES: 30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/588,128
FILING DATE: 24-SEP-1990
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 412,745
FILING DATE: 26-SEP-1989
APPLICATION NUMBER: 332,865
FILING DATE: 03-APR-1989
APPLICATION NUMBER: 176,532
FILING DATE: 01-APR-1988
SEQ ID NO: 2
LENGTH: 2039
5256642-2

Query Match 3.3%; Score 287.5; DB 6; Length 2039;
Best Local Similarity 19.1%; Pred. No. 4.8e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

221 LVLFASFEVPVT-EWVP-----RDE-----KYRLLEVLOGEPEPELISPLQPL-- 265
34 LALVVAAGQCAAPMLPAPARTNLDEPEPIGYLTAYECRPGSGRFSITICLKNSTWT 93
266 ---CGQTVCDN-----VELISQYNGYWPRLGEXVI 292
94 GAXDRCRRKSCRNPPDPVNGWVHIKIQFSGQIKYSTCKGRILIGSSASACIIISGDTVI 153
293 RYQVAVNICD--DEGLNPVSEBQIRLQHEALNEAF--SRYNISWQUSVHOVHNSITLHR 347
154 WDNETPICDRIPCGILPPTIT-----NDFISITNRENFY-----GS 189
348 VLVNVCESKIGND-----HDEPECHPLTGYDG---DCRLQGRCYSWNRBDGL 394
190 VVYTRCHPGSGGRVYFELVGEPSIYCTISNDQ--VGIMSGAPQCIIPNKCTPPNVEKGI 247
395 CHVECNMM--LNDPDDGC-----C-----DPQVADVKTCEPDSPKRAY 433
248 LVSDNRSLFSINVEVFRCPGVFVWKGRVYKCOALNKWBEPLPSGSRVCPDPDVLAHA- 306

434 MSVKELEALQINSTHF---LNIYFASSVREDLAGAATW-----PMDKQAVT----- 477
307 -----ERTORDKNFSPQGEVYVSCPEGYDLGASMRCTPGDWSAPAPTCBVXSCD 359
478 -----HGGIYLSAAYGMPDHTMTHEVGHVIG---LYHVFGK-----VSSRE 519
360 DFMQGLNGRLFPVNIQOLAKVDVFCDEGQQLGSSASVYVLGMSLNNSSVYVEQI 419
520 SCNDPCKEYVPS-METG-----DLCAD----- 540
420 FC--PSPVPIPNGRHTKPLEVPFPGKAVVYTCDPHDPDRTGSPILIGSTIRCTSDPGN 477
541 ---TAPTPKSEL---CEPE-----FTSDCGTRFP---GAFPTNMS 575
478 GWSPPAPRCGILGHCAPDHFLPAKTKOTNASDFIGTSLKCECREYVGRFS----- 533
576 YTDNCTDNF---TPNOVARMHCYLDLVQOQWTSRRTPIPIPMV----- 619
534 ---ITCIDNLVWSSPKVCK-----RKSCTPPDVNGWVHVTIDIOVGRIN 578
620 -----IGQTNKSLTI---HW--LPEI---SGVYDRASGSLCGACTEDGTFR 658
579 YSCTTGRIIGHSSAECILSGNAHMTKRPICQIPCGLPRTIANGDFI-----STNR 632
659 QYVHTAS--SRVCDSSGYWTPBEAVGPDPV---DOPEPSLOAMS--BEVHLHYMMN 709
633 ENFHYGVVYTRCNPGSGGRKRVFELVGEPSIYCTISNDQ---VGIMSGAPQCIIPNK 687
710 TVPCPTGCSLELLFQHPVQADTLTLWTSFFMESQVLFPTBILLE---NKESVHLGPT 766
688 CTPPNE-----NGLVSDNLSFSLNVEVFRCPQGVMMQGR 726
767 DTFCDIPILIKLHVDAVSGVYVTPDERIEIDALLTQSPHSLCSG--CAPRYQVLRD 825
727 RVKCO-----ALNKWBEPLPSGSRVCP----- 749
826 PPFASGLPVVYTHSHKFTDVE-VTPQOMYOYUOLANAGEL-GEAS---PRLNTHIGA 879
750 -----PPDLAHERQORDKNFSPQGEVYFS--CEPGYDLRGAAMRCTPGDWSPPAA 800
880 PYCG-----DGK---VSERLGEE---CDDGDLVSGDGS----- 907
801 PTCVKSCTDPMQGLNGRLVFPVNLQAKVDVFCDEGQQLGSSASVYVLGMSLNN 860
908 ---KVCE-----LE-----EGFNVCGEPSL-C 925
861 SSVPVCEQIFCPSPVPIPNGRHTKPLEVPFPGKAVVYTCDPHDPDRTGSPILIGESTIRC 920
926 YM-YEGDGI-----CE-----PEPKTSIVDCIYI---PKGY-- 954
921 TSDPQGGVWSSPAPRCGILGHCOAPDHPFAKTKYTINASDFIGTSLKYECPREYYGR 980
955 -----LDQATRAYSHED---KKKC--PVSIVTGEPSHIL-----CTSYHPD 992
981 PFSITICD--NLVWSSPKDYCKRKSCKTPDPVNGWVHVTIDIOVGRINYSTCTTH-R 1036
993 LPNHR-----PLTGWFPK---VASENETODDRSEOPGSLKKEDEV 1030
1037 LIGHSACILSGNTAMSTKPIQRIPCGLPRTIANGPFISTRNENFHYGV----- 1090
1031 WLKVCYFRPBEARAF-----IFLTIDG-----LVPEHQOPTYT--LYL 1068
1091 -VYTRCNLGSGRKRVFELVGEPSIYCTISNDQVIGSGAPQCIIPNKCTPPNVEKGI 1149
1069 TDVAGSNHSL-----GTYGLSCQ-----HNPLIIVYTHHQNVLFI 1103
1150 SD-----NRSLSFLNBEVVDPRCPGFVWKGRVYKCOALNKWBEPLPSGSRVCPPELILH 1205
1104 -HTTSVLNLFSSPBRVGISAVALTSTSRIGLSAPSNCISDEGQNHOGQSCIRHPCSKQ- 1160
1206 GEHTPSHQDNFSP-----GQEVFYSC--EPGYDLGASLH--CTPGG 1244
1161 -----DQPSILL--LDHADVVNCTISIGBLMKCAITQGRFALQASSQYIRPM 1207

Db 1245 DMSPEAPRCAYKSCDDFLGQLPHGKVLPLPLNLQLG-AKVSFVCDGKFLKSSVSH----- 1299
 Qy 1208 QKELLITSSSGHMDQNS-CLPVDGCVDPDLVANYANSSCSBG-TKFLKRSISICVP--- 1262
 Db 1300 ---CVLVGMRSLMNNSSVCEHIFCPNP-PAILNGRHGTSPSGDI PYGKEISYTCDDPAPD 1355
 Qy 1263 ---PAKLOGLSPLWLTCEDE---GLMSLPEVYCKL-----ECDAPIPLINANLLPHCLQ 1310
 Db 1356 RGMFENLIGEST-IRCTSDPHGNGVWSSPAPRCISLVAAGCKTPGQFPASPIIP--IN 1412
 Qy 1311 D-NHNDVGTICKYCKECPGYVAESABGKVRNKLKIQLCEGIWB--QGSCTIPVVCPPPP 1367
 Db 1413 DFEPPVGTSLNYECRPGYF-----GKMFSISCLLENLWSSVEDNCRKSCGPPPE 1462
 Qy 1368 VFEBCM-----VECTNGFSL---DSQCVLNCQBERKLPILCTKXGLWTOE 1469
 Db 1463 PFNGVHINTDTQSGSTVNYSCNBGFRLLIGSPSTTCLVSGNNV-----TWDKK 1510
 Qy 1410 FKLGENLOGECPPEPSELNS-----VEYKCEQGYG----- 1439
 Db 1511 APICEII--SCEPPTISNGDFYSNNRTSPHNGTVVYQCHTGPDDGQLFELVGERSTYC 1568
 Qy 1440 ---IGAVCSP-----LCVIPP-SDPVMLEPENT---ADTLEHMEP---VKV 1476
 Db 1569 TSKDQVGVWSSPPRCISTNKTCTAPAEVENAIRVGNRSFSLTEIIRFCQPGFVWVGS 1628
 Qy 1477 QSIYCTGRQWHDPVLVHICQSCER 1502
 Db 1629 HTVOCQINGRW--GPKLPHCSRVCP 1652

RESULT 12

5472939-2

Patent No. 5472939
 APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
 WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
 H.; MAKIDES, SAVVAS; MARSH, HENRY C. JR.
 TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
 MEDIATED DISORDERS
 NUMBER OF SEQUENCES: 30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/138, 825
 FILING DATE: 19-OCT-1993
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 588, 128
 FILING DATE: 24-SEP-1990
 APPLICATION NUMBER: 412, 745
 FILING DATE: 26-SEP-1989
 APPLICATION NUMBER: 332, 865
 FILING DATE: 03-APR-1989
 APPLICATION NUMBER: 176, 532
 FILING DATE: 01-APR-1988
 SEQ ID NO: 2:
 LENGTH: 2039
 5472939-2

Query Match 3.3%; Score 287.5; DB 6; Length 2039;
 Best Local Similarity 19.1%; Pred. No. 4.8e-15;
 Matches 349; Conservative 178; Mismatches 546; Indels 751; Gaps 105;
 Qy 221 LVLTASFEFVNT-EWVP-----RDE-----KYRLLEVLOGEPEPEELISPLQPL-- 265
 Db 34 LALVAVAMQCAPELPPARPTNLDEREPPIGYLANTECRPGYSGRFSLICLKNSVWT 93
 Qy 266 ---CGQTCGN-----VELISQYNGWPLRGKVI 292
 Db 94 GAKDRCRKRSCRNPPDPVNGMWHVYKIQSGSLKYCTKGRYLRISSASATCISGTVI 153
 Qy 293 RYQVAVTCD--DEGLNPVSEBQRLQHEALNEAF---SRYNIMQSLSVHQNHSITLRHR 347
 Db 154 WDNETPICDRIPCGLPPTT-----NGDFISTRENPHY-----GS 189

Qy 348 VLVNCEPSKIGND-----HCDPECEHPLTGYDGG---DCRLQRCYSWMNRDGL 394
 Db 190 VVTRYRCNPGSGKRVFELVGEPSIYCTSNDDQ--VGIMSGPAPQCIIPNKCTPPVWNGI 247
 Qy 395 CHVECNMM--LNPDDGDC-----C-----DPOYADVAKTFFDDSPGRAY 433
 Db 248 LVSDNRLFSLNVVERCQPVFMKGRPVKQALNKMPELPLSCSRVQCPDVLHA- 306
 Qy 434 MSYKELKALQLNSTH--LNIYFASVREDLAGAATW-----PMDKDAVT----- 477
 Db 307 -----ERTQRKDNFSPQGEVYFSGCEBGYDLRGAASNMCTPQGDMSRAPAPCEVYKSCD 359
 Qy 478 ---HLGGIVLSPAYYMGHTDTMIHEGVHLG---LYHVRKG-----VSERE 519
 Db 360 DFMQQLNGKRVLPVNLQLGAKVDVCDGEGQLKSSASCYLAAGMSLWSSVPCEQI 419
 Qy 520 SCNDPCKEYTPS--MENG-----DLCAD----- 540
 Db 420 FC--PSPVLPNGRHGTGKPLEVPPFGKAVNYTCDPHDRGTSPDLIGESTIRCTSDPQGN 477
 Qy 541 ---TAPPKSEL---CREPE-----PTSDTCGFTPEP--GAPFTNYS 575
 Db 478 GWMSSPAPRCGIIIGHCOAPDHPFLPAKLTQTNASDPFISLKYECREYGRPFS- 533
 Qy 576 YTDNCTDNF--TPNQVAMHCYLDLVYQWTESRKPPIPIPMV----- 619
 Db 534 ---ITCLDNLWSSPKOVCK-----RKSCTPPDPVNGMWHVITDIQVGSRLN 578
 Qy 620 -----IGQNKSLTI-----HW--LPI-----SGVYVRASGSLGACTBOSTR 658
 Db 579 YSCCTGRLIGHSSAECTISGNAAHMSTKPIICQRIPCGLPPTIANGDPI--STNR 632
 Qy 659 QYVHTAS--SRRYCDSGYWTPPEAVGPPDV-----DQCEPSLOAMS--PEVHLYHMM 709
 Db 633 ENFHYSVTRYRCNPGSGKRVFELVGEPSIYCTSNDDQ-----VGIMSGPAPQCIIPNK 687
 Qy 710 TVPCPTGEGSLLELFOHPVQADTLTLMWTSFFMESSQVLEFTEILLE--NKESVHLGL 766
 Db 688 CTPEPNV-----NGILVSDNRSLFSLNEVFEFRQCPFGVMGPR 726
 Qy 767 DTFCDDIPLTIKHAVDGVSGVKTTPDERIEIDAALLTSGPHSLCSG--CRPRVYQVLRD 825
 Db 727 RVKQ-----ALNKMPELPLSCSRVCP----- 749
 Qy 826 PPFASGLPVVVTSHRFTDVE--VTPQOMYQYVLAAGSEL--GEAS-----PPLNHTIGA 879
 Db 750 -----PPDVLAERTQRKDNFSPQGEVYFVS--CEPGYDLRGAASNMCTPQGDMSRA 800
 Qy 880 PYCG-----DGK-----VSERLGEE-----CDDGDLVSGDGS----- 907
 Db 801 PTCSEVSCDDFMQQLNGKRVLPVNLQLGAKVDVCDGEGQLKSSASCYLAAGMSLWN 860
 Qy 908 ---KVCE-----LE-----EGFNCVGEPSL-C 925
 Db 861 SSVAVCEQIIFCPSPVLPNGRHGTGKPLEVPPFGKAVNYTCDPHDRGTSPDLIGESTIRC 920
 Qy 926 YM-YEGDGI-----CE-----PFEKRTSIVDCGIYT-----PKGY-- 954
 Db 921 TSPDQNGVWSSPAPRCGIIIGHCOAPDHPFLPAKLTQTNASDPFISLKYECREYGR 980
 Qy 955 -----LDQWATRAYSHED--KKKC--PVSIVTGEPSHLI-----CTSYHPD 992
 Db 981 PFSITCLD---NLWMSSPKDVCKRKSCKTPPDPVNGMWHVITDIQVSRINYSCTTGH-R 1036
 Qy 993 LPMHR-----PLTGMFPC-----VASEHETQDDSEQPEGSLKXDEV 1030
 Db 1037 LIGHSSAECTISGNTAHTMSTKPIICQRIPCGLPPTIANGPFISTRNENHYGSV----- 1090
 Qy 1031 WLKVCENRPGEARAIF-----IFLTDDG-----LVGEHQOQPTVT--LYL 1068
 Db 1091 -VTRYCNLSGRKRVFELVGEPSIYCTSNDDQGIWSGAPACQIIPNKCTPPVWNGIIV 1149
 Qy 1069 TDVRGSNHSL-----GTGLSQC-----HNPLIIVTTHQNVLFH 1103

```

Db      1150 SD-----KSLFSLNEVDFRCQPRVGMKPRRVRKCOALNKMBELPSCSRVCOPEPILH 1205
Qy      1104 -HTTSLVILNFSPPRVGISAVALTSTSRIGLSAPNSCISEDEQNHQSCIRHPCGKO- 1160
Db      1206 GEHTPSHDNFS-----GQEVFYS-EPGYDLRGAALSH-CTPQG 1244
Qy      1161 -----DQPSLL-1DHADVNCSTISIGPLMKCAITTCQGFPLQASGQYIRPM 1207
Db      1245 DWSEAPRCAYKSCDDFLGQLPHGRVLPPLMLQLG-AKVSFVCEGFLKGSVSH----- 1239
Qy      1208 QKEILLTSSGHWQONVS-CLPVDGVPDPSLVVYANFSCSEG-TKFLKRSISCV- 1262
Db      1300 ---CVLVKMSLNNNSVPCHEIFCPNP-PAILNRRHTGTPSGDIPYKKEISTYCDPRPD 1355
Qy      1263 ---BAKLQGLSPWLTCLD---GLMSLPEVYCKL---ECDAPIILNANLLPHCLQ 1310
Db      1356 RGMTFNLIGEST-IRCTSDPHNGVWSSPAPRCBELSVAGCKTPEQFPFASPTIP-IN 1412
Qy      1311 D-NNDVGTICKYCKECPGYVABSAEGKVRANKLKIQCLEGGIWE--QGSCTPVCPEPP 1367
Db      1413 DPEEPVGTSLNYECPGYF-----GKWFISISCLNLSVSSVEDNCRKRKSGCPPPE 1462
Qy      1368 VEEGK-----YECTNGFSL-----DSQCVLNCQNEKXLPILCTKGLWTOE 1409
Db      1463 PFNGMVAINTDTQSGSTVYNSCNSGFLKISGSPSTICLVSGNNV-----TMDK 1510
Qy      1410 PKLCENTLOGECPPEPSELNS-----VEYKCEQGYG----- 1439
Db      1511 APICEII--SCPEPTISGDFYSNNRTSPFNHGTVVYTCQHTGPDGQLFELVGBRSIYC 1568
Qy      1440 -----IGAVCSP-----LCVIPP-SDPYMLPENIT---ADTLEHMEP---YKV 1476
Db      1569 TSKDDQGVWSSPPRCISTNKCTAPVEYNAIRVGNRSPSLTEIIRFCQGFVWGS 1628
Qy      1477 OSIIVTGRORHPDPVLVHCIOSECP 1502
Db      1629 HTVOCQTNGRV--GPKLPHCSRVCP 1652

RESULT 13
5256642-2
; Patent No. 5256642
; APPLICANT: FEARON, DOUGLAS T.; KLICKSTEIN, LLOYD B.; WONG,
; WINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IP, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: COMPOSITIONS OF SOLUBLE COMPLEMENT
; RECEPTOR 1 (CR1) AND A THROMBOCYTIC AGENT, AND THE METHODS OF
; USE THEREOF
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/588,128
; FILING DATE: 24-SEP-1990
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 412,745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332,865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176,532
; FILING DATE: 01-APR-1986
; SEQ ID NO: 2:
; LENGTH: 2039
5256642-2

Query Match 3.3%; Score 287.5; DB 6; Length 2039;
Best Local Similarity 19.1%; Pred. No. 4,8e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

```

```

Db      94 GAKRCKRKSRNPPDPVNGMNVHVIKGIQESQIKYCTCKYRLIGSSSACIIISGDTVI 153
Qy      293 RYQVNI CD--DEGLNPIVSEEOIRLOHEALNEAF---SRYNISQWSVHQVHNSTLRHR 347
Db      154 WNETPICDRIPCLPPTIT-----NGDFISTNRENFHY-----GS 189
Qy      348 VLVVNCERPSKIGND-----HCDPECEHPLTYDGG---DCRLQRCYSNNRBDGL 394
Db      190 VVTVRCNPGSGGRVFLVGBPSIYCTSNDDQ--VGISGAPQCIIPNCKTPPNVZGI 247
Qy      395 CHVECNMM--LNDPDDDC-----C-----DPQVADVKTCPDPSPKRAY 433
Db      248 LVSNRBLPSLNEVVERRCQPVFMKGRPRYKCOALNKMBELPSCSRVCOPEPDLHA- 306
Qy      434 MSYKELKALQLNSTHF--LNIYFASVREDLAGAATW-----PMDKAVT----- 477
Db      307 -----ERTQDRDNFSPQGEVIFYSCPEGYDLGAASMRCTPQGDWSPAAPTEVKS CD 359
Qy      478 -----HLGIVLSAAYYGMEGHTDTMHEVGVLG---LHVFKG-----VSERE 519
Db      360 DFMGQLNGRVLFEVNLQAKVDVFCDEGFQKSSASVCLAGMSLNNSSVPCEQI 419
Qy      520 SCNDPCKEIVPS-WETG-----DLCAD----- 540
Db      420 FC--PSPPVLPNGHHTGKPLEVFPFGKAVNTCDPHDRGTSFPLIGESTIRCTSDPOGN 477
Qy      541 ---TAPPKSEL---CREPE-----PISDTGFTTRP--GABFTYMS 575
Db      478 GWSPPAPRGILHCOAPDHPFLAKLKTQTNASDPITGSLKCECREYVGRFSS----- 533
Qy      576 YTDNCTDNF---TPNOYARMCTLDLVYQOMTSKRPPIPIPPV----- 619
Db      534 ---ITCDNLVWSSPKOVCK-----RKSKCTPPDPVNGMNVHVIIDIOVSRIN 578
Qy      620 -----IGQTKSLTI-----HW--LPII-----SGVYDDASGSLCAGATEDGTFR 658
Db      579 YSCITGHRILGHSAECILSNAAMHSTKPPICQIRICGLPPTIANGDFI-----STNR 632
Qy      659 QYVHTAS--SRVCDSSGYWTPBEAVGPDPV-----DQCPESLQWS--PEVHLYHNM 709
Db      633 ENFHYGSVVTYRCNPGSGGRKVFELVGBPSIYCTSNDDQ-----VGISGAPQCIIPNK 687
Qy      710 TVPCPTGCSLELLPQHPVADTLTLWTSFEMSSQVLPTEILLE---NKEVHIGPL 766
Db      688 CTPEPNEV-----NGLVSDNLSLSLNEVFERCQPGFVMGPR 726
Qy      767 DTFCDIPLTIKLHVDKSVGVKYVTPDRIEIDALLTTSOPHSPLCSG-CRPVRYQVLRD 825
Db      727 RVKCO-----ALNKMBELPSCSRVCP----- 749
Qy      826 PPFASGLPVVVTSHRKTDE--VTPQOMYOQVLAAGBEL-GEAS---PRLNHTIGA 879
Db      750 -----PPVLAHERQORDXNFSPPQEVFYS--CEPGYDLRGAASMRCTPQGDWSPA 800
Qy      880 PYCG-----DGK-----VSRLEGE---CDDGLVSGDGS----- 907
Db      801 PTCVKS CDDFMGQLNGRVLFPVNLQAKVDFVCEGFQKSSASVCLAGMSLNN 860
Qy      908 ---KVCR-----LE-----EGFNCVGBPSL-C 925
Db      861 SSVPVCEQIFCPSEPPVLPNGRHGKPLEVFPFGKAVNTCDPHDRGTSFPLIGESTTRC 920
Qy      926 YM-YEGDGI-----CE-----PPEKTSIYDCGIY-----PKGY- 954
Db      921 TSDPQNGVWSSPAPRGILGHCOAPDHPFLAKLKTQTNASDPITGSLKCECREYVGR 980
Qy      955 -----LDQWATRAYSSHED---KKKC--PVSLVTGEPHSLI-----CTSYHPD 992
Db      981 PFSITCLD---NLWSSPKDVCKRKSCTPPDPVNGMNVHVIIDIOVSRINYSCTTGH-R 1036
Qy      993 LPNHR-----PLTGWFPK-----VASEMTEQDRSEBOEGSLKKXDEV 1030

```

```

Db 1037 LIGSSAECISGNTAMSTKPCICORIPCGLPPIANGDFISTNRENFHYSV----- 1090
Qy 1031 WLKCCFNRPGARAF-----IFLPTDS-----LVPGHQPTT--LYL 1068
Db 1091 -VTVRCVLSGRKRVFELVGPSTICTSNDQVIGSGPAPQCIIPNKCTPPNVEINGILV 1149
Qy 1069 TDVAGSNHSL-----GTGGLSCQ-----HNPLIINTVTHHQNVLFI 1103
Db 1150 SD-----KSLFSLNLEVDVFCQPGFVWKGPRRVACQALNKWPELPSCSRVCPPELILH 1205
Qy 1104 -HTTVSLANFSSRPVIGSAVALRTSSRIGLSAPSNCSISEDEGQNHQOCSTIRPPCQK- 1160
Db 1206 GEHPSHQDNFSP-----GQEVFYSQ--EPGYDLGGAASLH--CTPOG 1244
Qy 1161 -----DSCPSLL--LDHADVYVNCSTIGPLMKCAITCGRFALOASSQGYLRPM 1267
Db 1245 DWSBPAPRCVAVKSCDDEFGQLPHGRVLPPLNLQUG-AKVSVFVCDGFRLLKSSVSH----- 1299
Qy 1208 QKEILLTCSGSHMDQNV-CLPVDGVPDPSPSLVNVANFSCSEG-TKFLKRCSTSCVP-- 1262
Db 1300 ---CVLVGMRSLMNSVPCVCEHIFCPNP-PALINGRHGTGPSGDIPIYKEISTYCDPHPD 1355
Qy 1263 ---PAKIQGISPWLTCLD---GLWSLPEVYCKL---ECDAPPIILNANLILPHCLQ 1310
Db 1356 RGMTFNLIGEST-IRCTSDPHGNGVWSSPAPRCCLSVRAGHCKTPEQPPFASPPIP--IN 1412
Qy 1311 D-HNDVGTICVKECKPGYVAESAAGKVRNKLKICLEGIME--QSSCIPVVCCEPPP 1367
Db 1413 DFEFVGTSLNVECRPGYF-----GMPFSISCLLENLWSSVEBCKRKSCKGPPPE 1462
Qy 1368 VFEGM-----YECTNGFSY---DSQCVLNCSQERKPLILCTKEGLWTQE 1409
Db 1463 PFNMGVHINTDTQGSTVNVSCNEGFRLLIGSPSTTCLVSGNNV-----TMDKK 1510
Qy 1410 FKUCENIQCCEPPPSSELAN-----VEYKEQGYG----- 1439
Db 1511 APICEII--SCPEPPIISNGDFYNNRTSPFNNGTVVYQCHTGPDGOQLFELVGERSIYC 1568
Qy 1440 -----IGAVSCP-----LCVLP-SDPVMLEPENT---ADTLEHMMEP---VKV 1476
Db 1569 TSKDOYGVWSSPPRCISTNKTCTAPEVENAIRVGNRSFSLTEIIRFCQPGFVWGS 1628
Qy 1477 QSIVCTGRQWHPDPVLVHCIOGCEP 1502
Db 1629 HTVOCQNGRW--GPKLPHGSRVQCP 1652

RESULT 14
5472939-2
; Patent No. 5472939
; APPLICANT: PEARON, DOUGLAS T.; KLOCKSTEIN, LLOYD B.; WONG,
; MINNIE W.; CARSON, GERALD R.; CONCINO, MICHAEL F.; IR, STEPHEN
; H.; MAKRIDES, SAVVAS; MARSH, HENRY C. JR.
; TITLE OF INVENTION: METHOD OF TREATING COMPLEMENT
; MEDIATED DISORDERS
; NUMBER OF SEQUENCES: 30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/138, 825
; FILING DATE: 19-OCT-1993
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 588, 128
; FILING DATE: 24-SEP-1990
; APPLICATION NUMBER: 412, 745
; FILING DATE: 26-SEP-1989
; APPLICATION NUMBER: 332, 865
; FILING DATE: 03-APR-1989
; APPLICATION NUMBER: 176, 532
; FILING DATE: 01-APR-1986
; SEQ ID NO: 2:
5472939-2

```

Query Match 3.3%, Score 287.5, DB 6, Length 2039;

```

Best Local Similarity 19.1%; Pred. No. 4, 8e-15;
Matches 349; Conservative 178; Mismatches 548; Indels 751; Gaps 105;

Qy 221 LVLTASREPVNT-EMVPF-----RDE-----KYRLBVLQGFEPPELISLQPPY-- 265
Db 34 LALPVAMGQCNAAEMLPFAPATNLTDPEFPITGTLYNVECRPGISGRPSIILCKKSVWT 93
Qy 266 -----CGQTVCDN-----VELISQYNGWYPLRGKVI 292
Db 94 GARDRCRKSCKRPPDPVNGMVAHVIQIGQSGIKYSCWKGYRLIISSSATCIIISGDTVI 153
Qy 293 RYGVVNICD--DEGLNPIVSEBQIRLOHEALNAF--SRYNISWQLSVQVHNSITLRHR 347
Db 154 MDNETPICDRIIPGCLPPTIT-----NDDFISTNRENFHY-----GS 189
Qy 348 VVLVNEBPSKIGND-----HDDPEGEHPLTGYDG--DCRLQRCYSMNRRDL 394
Db 190 VVTVRCNPGSGGKRVFELVGPSTICTSNDQ--VGWSGPAPQCIIPNKCTPPNVEINGI 247
Qy 395 CHVECNMM--LNDPDDGDC-----C-----DPOVADVKTCTFDDSPKRAY 433
Db 248 LVSDNKSFLSLNVEVERQCPVFMGPRRVKQALNKWPELPSCSRVCPPEPDLVHA- 306
Qy 434 MSVKELEKALQINSTHF--LNIYFASVREDIAGAATW-----PMDKQAVT----- 477
Db 307 -----ERTQRDKDNFSPQEVFVYSCPEGYDLRGAAISMCTPQGMSPAPPTCEVKS 359
Qy 478 -----HGGIVLSPAYYGMGHTDTMINEVGHUG--LVHVPKG-----VSERE 519
Db 360 DFMGQLNGRVLPPVNLQUGAKVDFVCDGFGQKSSASVCLVAGHESLMSVPCEQI 419
Qy 520 SCNDPCKETVPS-METG-----DLCAD----- 540
Db 420 FC--PSPFVLPNGRHGKPLEVFPFGKAVNYTCDPHDRGTSFDLIGESTIRCTSDPGCN 477
Qy 541 ---TAPPKSEL--GREP-----PTSDTCGTPRP--GAPFTNYS 575
Db 478 GWSSPAPRCGIIHGQAPDHPFLAKIKQTINASDPITGISTLYEBCRPVYGGPFS-- 533
Qy 576 YTDNCTDNF---TPNOVAMHCYLDLVVQWTESRKPPIPIPMV----- 619
Db 534 ---ITCLDNLWSSPDDVCK-----RKSKCTPPDPVNGMVAHVTIDQVGRIN 578
Qy 620 -----IGQTNKSLTI-----HW--LPPI-----SGVYDRASGLGACTEDGTFR 658
Db 579 YSCTGHRHLGHSABECILSGNAHWSKRPICGRIPCGLPPIANGDFI-----STNR 632
Qy 659 QYVHTAS--SRVCDSSGVTTPBEAVGPPV-----DQCEPSLOAMS--PZYHLTHMM 709
Db 633 ENFHYSGVVTVYRCNPGSGGRKRVFELVGPSTICTSNDQ-----VGWSGPAPQCIIPNK 687
Qy 710 TVPCPTGEGSLLELPHQPVADLTLLWVSFFMSSQVLDTEILLE--NKESVHLGPL 766
Db 688 CTPEPNE-----NCILVSDNLSFLSLEAVEFRQCPGVWKGPR 726
Qy 767 DTFCDIPILIKLHVDKSVGVKYVTEPDERIEIDALLTSQPHSPISG--CRPVRYOVLAD 825
Db 727 RVACQ-----ALNKWPELPSCSRVQCP----- 749
Qy 826 PPSASGLPVVYVTHSRKFTDVE--VTPOGMQYOVULAAGEEL-GEAS-----PRLNTHIGA 879
Db 750 -----PPVLHAERTQORDKNFSPQEVFYS--CEPGYDLGGAASMRCTPQDWSPPAA 800
Qy 880 PYCG-----DGK-----VSERLGE-----CDDGDLVSGDGS----- 907
Db 801 PTCVKSCDDFMQQLNGRVLFPVNLQUGAKVDFVCDGFGQKSSASVCLVAGHESLMM 860
Qy 908 ---KVCE-----LE-----EGNVCYGEPSL-C 925
Db 861 SSVPVCEQIRCPRPVLPNGRHGKPLEVFPFGKAVNYTCDPHDRGTSFDLIGESTIR 920
Qy 926 YM-YEGDGI-----CE-----PPEKTSIVDCGIYT-----PKY-- 954

```

```

Db      921 TSDQNGCWSSPAPRCGLGHQAAPHFLAKLTQTNADPRTGSLKCEPRYYGR 980
Qy      955 -----LDQWATRAYSSHD---KKKC--PVSLVTGEPHSLI-----CTSYHPD 992
Db      981 PFSITCLD---NLVWSSPKDVCKRKSCTPPDPVNGMHVITDIQVGSRIYSCCTGH-R 1036
Qy      993 LPMNR-----PLTGMFPC-----VASENETQDRSREPGSLKKEDEV 1030
Db      1037 LIGHSSABCLISGNTAHMSTKPCQRIPCGLPPTIANGDPISTNRENFHYGV----- 1090
Qy      1031 WLKCFNRPGRBARAIF-----IFLTLDG-----LVPGHQOQPTV--LYL 1068
Db      1091 -VTRCULGSKRGKVFELVGEPSIYCTSNDDQVIGMSPARQCIIPNKCTPTNENGILV 1149
Qy      1069 TDVRSNHSI-----GTVGLSCQ-----HNPLIINVTHHQNVLFH 1103
Db      1150 SD-----NRSLSFLNEVDPRCQPGFVMKPRRVKQALNKMPELPSCSRVCQPPRLIH 1205
Qy      1104 -HTTSVLNASSRVRGSAVALRTSSRIGLSAPSNCSSEDEGQNHQGSQIHRPCGQ- 1160
Db      1206 GEHTPSHODNFS------GQEVFVSC--EPGYDLRGAASLH--CTPQG 1244
Qy      1161 -----DSCPSLL--LDHADVNCSTSIGPLMKCAITTCQGFALQASGQYRPM 1207
Db      1245 DMSPEARCAVKSDDPLGOLPHGRVLPFLNLQIG-AKVSFVCEBGRFLKSSVSH----- 1239
Qy      1208 QKEILLTCSGHWQDONS-CLPVDGVPDPSLVNANFSCSEG-TKFLKRCISICVP--- 1262
Db      1300 ---CVLGMRSJLMNNSVAVCEHIFCPNP-PAIINGRHGTGSDIPIYCKEISYTCDFHPD 1355
Qy      1263 ---PAKQGLSPMLTCLD---GLMSLPEVYCYL---ECDAPPIIANLPHCLQ 1310
Db      1356 RGMTFNLIGEST-IRCTSDPRHNGWSSPAPRCBLSVAGHCKTPEOPFPASPTIP--IN 1412
Qy      1311 D-NHDVGTICYECKPGYVVASAEGKVRNKLKIQCLEGGIWE--QSCCTPVVCEPPPP 1367
Db      1413 DFEFVGTSLNTECRPGTF-----GKMPSISCIENLVWSSVEBNCRKSCGPPPE 1462
Qy      1368 VFEGM-----YECTNGFSL---DSQCVLNCQBERKLPILCTKEGLWTQ 1409
Db      1463 PFMGMVHINTDTQGSTVYNVSCNEGFRILGSPSTCLVSGNNV-----TWDKK 1510
Qy      1410 PKLCENIQEGCPPRPSSELS-----VEKCEQGYG----- 1439
Db      1511 APICEII--SCBPPTISNGDFYSNNRTSPFNGTVVYQCHTGDGRLFELVGERSIYC 1568
Qy      1440 ---IGAVCSP-----LCVIPP-SDPVLMPENIT---ADTLEHMMER---YKV 1476
Db      1569 TSKDDQVWSSPPRCISTKCTAFAVENAIRVGNRSFSLTEIIRFCQPGFVWGS 1628
Qy      1477 QSIIVCTGRQWHPDPVLVHCIOGCEP 1502
Db      1629 HTVQCQTNGRW--GPKLPHCGRVQCP 1652

```

```

; PRIOR FILING DATE: 1996-07-15
; NUMBER OF SEQ ID NOS: 53
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 52
; LENGTH: 1947
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: CRI
US-09-612-314A-52

Query Match      3.3%; Score 287; DB 4; Length 1947;
Best Local Similarity 19.1%; Pred. No. 5e-15;
Matches 346; Conservative 176; Mismatches 541; Indels 750; Gaps 104;

Qy      233 EWVFF-----RDE-----KYRLEVLQGFBEPELISLPQPL-----CGQTVCDN 273
Db      6 EMLPFAPTNLDTBEFPIGTIYNBECRPGISGFRFIIICKXSVWTKGAKDRCKRKSGRN 65
Qy      274 -----VELISQYNGYMPLRGKQIRYOVNIGD--DE 303
Db      66 PDPVNGMVHVIKIGIQFSQIKYSCTKGYRLIGSSSATCIISGDTVIMDETPICDRIPC 125
Qy      304 GLNPVSEEQIRLOHEALNEAF---SRVNTSMQLSVHQVNSTLRHVVLVNCSPSKGN 360
Db      126 GLPPTIT-----NGDFISTNRENFHY-----GSVVTRCRNPSGGR 161
Qy      361 D-----HCPRECEHPLTGYDGG---DCRLQGRCSWMRRDGLCHVECNM--LND 405
Db      162 KVFELVGEPSIYCTSNDDQ--VGIGMSPARQCIIPNKCTPTNENGILVBDNRSLFSLNE 219
Qy      406 FDDGDC-----C-----DPOVADVRKTCFDDPSPRAYMSKELKALQLN 446
Db      220 VVEFRQCPGFVMKPRRVKQALNKMPELPSCSRVCQPPDVLHA-----ERTQD 271
Qy      447 STFR---LNTYFASVREDLAAGATW-----PMDKQAVT-----HLGIVLS 485
Db      272 KDNFSGQEVFVSCPEGYDLRGAASMRCTPOGDMSPAPATCEVKSDDPFKQNLNGLRFL 331
Qy      486 PAVYGMFGHTDTHIEVGVIG--LYHVEFG-----VSERESCDNPKCEYVPS- 531
Db      332 PVLNLQAKVDFVDEBQFOLKSSASCYVLAMESLWNSVVPVEQIFC--PSPVYIPNG 389
Qy      532 METG-----DLCAD-----TAPYKSEL- 549
Db      390 RHTEKPLEVFPFGKAVNYTCDPHPRDRTSFDLIGESTIRCTSPDQNGWSSPAPRCGIL 449
Qy      550 --CREP-----PTSDTCGTPRP--GAPFTNVMYTDNDCTDNF--- 585
Db      450 GHCQAPDHLFLAKLTQTNASDPFICTSLKCEPRYYGRFS-----ITCLDNLWMS 502
Qy      586 TPNOVARMHCYLDLVYQWTESRKRPPIPIPMV-----IGQT 623
Db      503 SPKDVCK-----RKSKCTPPDPVNGMHVITDIQVGSRIYSCCTGHRLLGHS 550
Qy      624 NKSITTI---HW--LPEI-----SGVVYDRAAGSLGACTDGTFRQVYHTAS--SRV 669
Db      551 SAECIIISGNAAHMSTKPCQRIPCGLPPTIANGDFI-----STNRENFHYGSVTVYRC 604
Qy      670 CDSSGYTPREAVGPRPV-----DQCEBSIQAMS--PEVNLHYMMNTVPCPTGSCLEL 722
Db      605 NPSGGRKVFELVGEPSIYCTSNDDQ-----VGIGMSPARQCIIPNKCTPTNVE----- 653
Qy      723 LFGHPVQADTLTLMVTSFFMSSQVLEFTEILLE--NKESVHLGRLDTFCDLPLTIKIH 779
Db      654 -----NOLIVSDNRSLFSLNBYVEFRQCPGFVWKKGRPVVQ----- 690
Qy      780 VDGKVGSKVYTYTDERIEIDALLTSQPHSPLCSG--CRPVRYOVLNDRPPASGLPVVYTH 838
Db      691 -----ALNKMEPELPSCSRVCQP-----PDDVLH 714
Qy      839 SHRKFTDVE--VTRGQMYQYOVLAAGEEL--GEAS-----PRLNHHGAPVYG----- 883

```

Db 715 AERTQRDKDNFSPQGEVFFYS--CEPGYDLRGAASMRCTPGQDWSPPAAPTCEVKS CDDFMG 772
QY 884 ---DGK---VSERLGEE---CDDGLVSGDGS-----KVCB----- 911
Db 773 QLINGRVLPVNLQLGAKVDFVCEGFQLKSSASAYCVLAGMESLWNSVAVCEQIFCPS 832
QY 912 -----LE-----EGFNVCGEPSL-CYM-YEGDGI----- 933
Db 833 PPVLPNGRHGKPLEVPPFGKAVNYTCDPHRDGTSFDLIGESTIRCTSDPDQNGVWSSP 892
QY 934 -----CE-----PPEKTSIVDCGIYT-----PKGY-----LDQWATR 961
Db 893 APRCGIIGHQAPRHPFLPAKLTQTNASDPFISLKYECRPEYGRPFSTICLD---NL 949
QY 962 AYSHED---KKK---PVSLVTGEPHSLI-----CTSYHPLDPNHR----- 997
Db 950 VMSSPKDVCKRKSCKTPDPVNGMVHVTDIQVGRINYSCTTGH-RLIGHSSAECILSG 1008
QY 998 -----PLTGMFPC-----VASENETODDRSEQPEGSLSKKEDEVWLKVCFNRPGEAR 1043
Db 1009 NTAWMSTKPIICQRIPCGLPPTIANGDPISTNRNFHGSV-----VTRYCNLGSRGK 1061
QY 1044 AIF-----IFLTITDG-----LVPEHQOPTVT--LYLTVRGSNHSI--- 1078
Db 1062 KVFELVGEPSIYCTSDNDQVGIWSGAPQCIIIPNKTCTPPNVENGILVSD---NRSLSFL 1117
QY 1079 -----GTYGLSCQ-----HNPLIINVTHQNVLFH--HTTSVLNFPSS 1114
Db 1118 NEVEFRCPQPGFVWKGPFRVYCOALNKWEPELPSCSRVCOPPPRLHGEHTPSHODNFSF 1177
QY 1115 PRVGISAVALRTSRIGLSAPNSCTISEDEQNHQOSCIHRPCGKQ-----DS 1162
Db 1178 -----QGEVYFSC---EPGYDLRGAASLH--CTPGQDWSPEAPCAVKS 1216
QY 1163 CPSLL--LDHADVNTSGISGGLMKCAITCQGFALQASGQYIRPMCKEILLTCSSGHW 1220
Db 1217 CDDPLGQLPBGRVLPPLNLQIG-AKVSFVCEDEGFLKGSVSH-----CVLVGMRSLW 1268
QY 1221 DQUNS-CLPVDCGVPPDSLVVYVYANFSCSEG-TKFLKCSISCVP-----PAKIQGLSPW 1272
Db 1269 NNSVAVCEHIFCPNP-PAILNGRHGTGPSGDIPLYKELISTYCDPHPRGMTFNLIIGEST- 1326
QY 1273 LTCLED-----GLMSLPEVYCKL-----ECDAPILLNANLLPHCLD-NHDVGTICKYE 1322
Db 1327 IRTCTSDPHGNGVWSSPAPRCELSVRAGCKTPBQPPFASPTIP--INDFERPVGTSINYE 1384
QY 1323 CKPGYVAESAEGKVRNKLKIQCLEGTIME--QSCIPVVCPEPPPVFEGM----- 1372
Db 1385 CRPGYF-----GKMFISISCIENLWSSVEDNCRKSCGPPPEPFNGMVHINTDTQ 1434
QY 1373 -----YECTNGFSL---DSQCVLNCGQEREXLPILCTKEGLWTQERKLCENLQGECP 1422
Db 1435 FGSTVANSYCNBGFRLIGSPSTTCLVSGNNV-----TWDKAPICEIT--SCEP 1480
QY 1423 PSEELNS-----VEYKCEQGYG-----IGAVCSP 1446
Db 1481 PPTISNGDFYNNNTSFHNGTVVYYQCHTGPDSQQLFELVGERSIYCTSKDDQVWSSP 1540
QY 1447 -----LCVLP--SDPVLMPENIT---ADTLEHMEP---VKQOSIVCTGRQMP 1489
Db 1541 PPRCISTNKCTAPVEVNAIRVPGNRSFSLTEIRFCQPGFVWVGSHTVQCQTNGRW-- 1598
QY 1490 DPVLVHCLQSCGP 1502
Db 1599 GPKLPHCSRVCP 1611

Search completed: August 25, 2005, 22:25:59
Job time : 47.5172 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 22:20:01 ; Search time 110.721 Seconds

(without alignments)
5529.033 Million cell updates/sec

Title: US-09-983-025b-2_COPY_234_1791

Perfect score: 8612
Sequence: 1 SPBPESQNGSGSYRAET.....AADCDLDECTCRPKAEENQ 1558

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1767149 seqs, 392926209 residues

Total number of hits satisfying chosen parameters: 1767149

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/prodata/2/pubppaa/PCT_NEW_PUB.pep.*
- 3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/prodata/2/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/prodata/2/pubppaa/PCTUS_PUBCOMB.pep.*
- 7: /cgn2_6/prodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/prodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/prodata/2/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/prodata/2/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep.*
- 13: /cgn2_6/prodata/2/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/prodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/prodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/prodata/2/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/prodata/2/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/prodata/2/pubppaa/US10_NEW_PUB.pep.*
- 19: /cgn2_6/prodata/2/pubppaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	8612	100.0	1791	10	US-09-983-025-2
2	8592	99.8	1791	9	US-09-827-998-3
3	8592	99.8	1791	15	US-10-675-685-3
4	8263	95.9	1770	9	US-09-827-998-10
5	8263	95.9	1770	15	US-10-675-685-10
6	6126	71.1	1385	9	US-09-827-998-16
7	6126	71.1	1385	15	US-10-675-685-16
8	3916.5	45.5	1627	10	US-09-983-025-25
9	3916.5	45.5	1627	15	US-10-295-027-663
10	3916.5	45.5	1627	17	US-10-783-311-1
11	3916.5	45.5	1627	17	US-10-741-600-1406

12	3916.5	45.5	1627	17	US-10-991-321-32	Sequence 32, App1
13	3916.5	45.5	1627	18	US-10-887-229A-8	Sequence 8, App1
14	3914.5	45.5	1547	17	US-10-783-311-2	Sequence 1403, App1
15	3602	41.8	1420	17	US-10-741-600-1403	Sequence 1403, App
16	3602	41.8	1420	17	US-10-741-600-1405	Sequence 1405, App
17	3044	35.3	1232	17	US-10-741-600-1404	Sequence 1404, App
18	2219	25.8	858	15	US-10-334-143-85	Sequence 85, App1
19	1893	22.0	704	17	US-10-741-600-1402	Sequence 1402, App
20	1086	12.6	192	9	US-09-864-761-34265	Sequence 34265, A
21	383	4.4	70	9	US-09-864-761-34264	Sequence 34264, A
22	360.5	4.2	165	9	US-09-864-761-34263	Sequence 42873, A
23	346.5	4.0	3567	15	US-10-028-248A-47	Sequence 47, App1
24	346.5	4.0	3567	15	US-10-107-782-47	Sequence 47, App1
25	336.5	3.9	3594	16	US-10-603-283-2	Sequence 2, App1
26	336.5	3.9	3594	13	US-09-911-842-4	Sequence 4, App1
27	336.5	3.9	3594	13	US-10-150-821-4	Sequence 4, App1
28	334.5	3.9	3557	15	US-10-295-027-430	Sequence 430, App
29	334.5	3.9	3557	15	US-10-295-027-1297	Sequence 1297, App
30	332.5	3.9	3568	15	US-10-028-248A-8	Sequence 8, App1
31	332.5	3.9	3568	15	US-10-107-782-8	Sequence 8, App1
32	332.5	3.9	3570	15	US-10-028-248A-6	Sequence 6, App1
33	332.5	3.9	3570	15	US-10-107-782-6	Sequence 6, App1
34	330.5	3.8	3571	9	US-09-911-842-2	Sequence 2, App1
35	330.5	3.8	3571	13	US-10-150-821-2	Sequence 2, App1
36	324	3.8	63	9	US-09-864-761-34262	Sequence 34262, A
37	287.5	3.3	2039	17	US-10-741-600-1241	Sequence 1241, App
38	287.5	3.3	2044	15	US-10-276-774-2152	Sequence 2152, App
39	287	3.3	1947	16	US-10-742-887-52	Sequence 52, App1
40	284	3.3	2489	9	US-09-911-842-5	Sequence 5, App1
41	284	3.3	2489	13	US-10-150-821-5	Sequence 5, App1
42	284	3.3	2489	17	US-10-741-600-1242	Sequence 1242, App
43	284	3.3	3564	15	US-10-016-248-45	Sequence 45, App1
44	283	3.3	1139	9	US-09-764-893-102	Sequence 102, App1
45	283	3.3	1139	9	US-09-764-881-99	Sequence 99, App1

ALIGNMENTS

RESULT 1
US-09-983-025-2
Sequence 2, Application US/09983025
Publication No. US20030124529A1
GENERAL INFORMATION:
APPLICANT: OXVIG, Claus
TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)
FILE REFERENCE: OXVIG-1A
CURRENT APPLICATION NUMBER: US/09/983, 025
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/241, 840
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: DK PA 2000 01571
NUMBER OF SEQ ID NOS: 25
SOFTWARE: Patentin version 3.1
SEQ ID NO 2
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(66)
OTHER INFORMATION: prepro part of PAPP-A2
NAME/KEY: misc_feature
LOCATION: (67)..(699)
OTHER INFORMATION: pro part of PAPP-A2
US-09-983-025-2
Query Match 100.0%; Score 8612; DB 10; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 SPPEBSONGEGSYREAEFTNSQVGLPILYFSGRREBRLLRPEVLAIEIPREAFVTEAWV 60
DB 234 SPPEBSONGEGSYREAEFTNSQVGLPILYFSGRREBRLLRPEVLAIEIPREAFVTEAWV 293
QY 61 KPEGGONNPALIIAGVFNCSHTVSDKGWALGIRSGKDGKRDARFFPSLCTDRVKKATIL 120
DB 294 KPEGGONNPALIIAGVFNCSHTVSDKGWALGIRSGKDGKRDARFFPSLCTDRVKKATIL 353
QY 121 ISHSRYOPGTWTHVAATYDGRHMAIYVDGTQVASSLDOSGPLNSPFMA5CRSLLGGDS 180
DB 354 ISHSRYOPGTWTHVAATYDGRHMAIYVDGTQVASSLDOSGPLNSPFMA5CRSLLGGDS 413
QY 181 EDGYFRGHGLTILVFWSTALPOSHFOHSSOHSGBEERATDLVLTASFEVNTWVPFRDE 240
DB 414 EDGYFRGHGLTILVFWSTALPOSHFOHSSOHSGBEERATDLVLTASFEVNTWVPFRDE 473
QY 241 KYPRLEVLQGFEPPEILSPLOPPLCGQTVCDNVELISQYNGWPLRGEKVIYQVNNIC 300
DB 474 KYPRLEVLQGFEPPEILSPLOPPLCGQTVCDNVELISQYNGWPLRGEKVIYQVNNIC 533
QY 301 DDEGLNPIVSEBQIRLOHEALNEAFSRNYSWOLSYHOVNSTLRHRYVLTNCEPSKIGN 360
DB 534 DDEGLNPIVSEBQIRLOHEALNEAFSRNYSWOLSYHOVNSTLRHRYVLTNCEPSKIGN 593
QY 361 DHCPCEGHPILTYDGDGCRLOGRCSWNRDGLCHVECNMMLNDFDDGDCDQVADVR 420
DB 594 DHCPCEGHPILTYDGDGCRLOGRCSWNRDGLCHVECNMMLNDFDDGDCDQVADVR 653
QY 421 KTCFDPSPKAYMSVKEKALQJNSTHFNITFYASVREBLAGAATWPKDAVTHLG 480
DB 654 KTCFDPSPKAYMSVKEKALQJNSTHFNITFYASVREBLAGAATWPKDAVTHLG 713
QY 481 GIVLSPAYGMPGHTDMIHVGHVGLYHFKVSEBESNDCKETVPMEMEGDLCAD 540
DB 714 GIVLSPAYGMPGHTDMIHVGHVGLYHFKVSEBESNDCKETVPMEMEGDLCAD 773
QY 541 TAPPKSELCREPTSDTCGFTFPGARFTNYSYTDNDCTDFTPNQVARMHCYDLY 600
DB 774 TAPPKSELCREPTSDTCGFTFPGARFTNYSYTDNDCTDFTPNQVARMHCYDLY 833
QY 601 YQOMTESRKPPIPIPMWIGQINKSLTIHMLPISGVVYDRA5GSLCGACTEDGTRQY 660
DB 834 YQOMTESRKPPIPIPMWIGQINKSLTIHMLPISGVVYDRA5GSLCGACTEDGTRQY 893
QY 661 VHTASSRRVCDSSGYMTPEEAVGPPVDQPCBPSLQAMSPVHLYHMMVTPCPTGCSL 720
DB 894 VHTASSRRVCDSSGYMTPEEAVGPPVDQPCBPSLQAMSPVHLYHMMVTPCPTGCSL 953
QY 721 ELRFQHPVQADTLTLMTWTSFPMESQVLPTEIILLENKESVHLGPLDTCDIPLTIKLV 780
DB 954 ELRFQHPVQADTLTLMTWTSFPMESQVLPTEIILLENKESVHLGPLDTCDIPLTIKLV 1013
QY 781 DGKVSQVYVTFDERIEIDALLTSOPHSPLCSGCRPVRYQVLDPPFASGLPVVYTHSH 840
DB 1014 DGKVSQVYVTFDERIEIDALLTSOPHSPLCSGCRPVRYQVLDPPFASGLPVVYTHSH 1073
QY 841 RKFPTDEVTEQOMYQVYLAAGELGASPLNHHIGAPCGGKTSERLGECCDDGDL 900
DB 1074 RKFPTDEVTEQOMYQVYLAAGELGASPLNHHIGAPCGGKTSERLGECCDDGDL 1133
QY 901 VSGGCGSKVCELEJEGFNCVGEPSLCMYEGDICEPFEKTSYVDCGIYTPKGLDOWAT 960
DB 1134 VSGGCGSKVCELEJEGFNCVGEPSLCMYEGDICEPFEKTSYVDCGIYTPKGLDOWAT 1193
QY 961 RAYSSHEDKXKCPVSLVTGEPHSLICTSYHDLPHNRPPLTGMPFVASENETQDRSEOP 1020
DB 1194 RAYSSHEDKXKCPVSLVTGEPHSLICTSYHDLPHNRPPLTGMPFVASENETQDRSEOP 1253
QY 1021 EGSJLKEDEWMLKCFNRPGEARAIPLFTLTDGLVPEHQOPTYTLTLTVRGSNHLG 1080
DB 1254 EGSJLKEDEWMLKCFNRPGEARAIPLFTLTDGLVPEHQOPTYTLTLTVRGSNHLG 1313
QY 1081 YGJSCQNPPLIINTVHHQNVLFHHTTSVLNFS5SPRVGISAVALTSSRIGL5AP5NCIS 1140

```

```

DB 1314 YGJSCQNPPLIINTVHHQNVLFHHTTSVLNFS5SPRVGISAVALTSSRIGL5AP5NCIS 1373
QY 1141 EDEGQNHQSGSCIHRCQKODSCPSLLLDHADVNTCSIGRGLMKCAITQGRPALQASS 1200
DB 1374 EDEGQNHQSGSCIHRCQKODSCPSLLLDHADVNTCSIGRGLMKCAITQGRPALQASS 1433
QY 1201 GQYIRPMQKEIILTCSSGHNDQNVSCIPIVDCGVDDSLVNYANFSCSEGTFLKRCISIC 1260
DB 1434 GQYIRPMQKEIILTCSSGHNDQNVSCIPIVDCGVDDSLVNYANFSCSEGTFLKRCISIC 1493
QY 1261 VPPAKLQGSPLWLTCELDGLMSLPEVYCKLECDAPPIILNANILLPHCLQDNHDVGITCK 1320
DB 1494 VPPAKLQGSPLWLTCELDGLMSLPEVYCKLECDAPPIILNANILLPHCLQDNHDVGITCK 1553
QY 1321 YECKPGYVAESAEGKVRNKLKIQCIEGSIWQSGCIPVCEBPPPVFEGMTECTNGES 1380
DB 1554 YECKPGYVAESAEGKVRNKLKIQCIEGSIWQSGCIPVCEBPPPVFEGMTECTNGES 1613
QY 1381 LDSQCVLNCQREKPLPILCTKEGLWTOEFKLQENIQCECPPEPSELNSVEYKCEQGYI 1440
DB 1614 LDSQCVLNCQREKPLPILCTKEGLWTOEFKLQENIQCECPPEPSELNSVEYKCEQGYI 1673
QY 1441 GAVCSPCLVIPSPDPVWLPENITADTLEHMEPVKYQSICTGRORWHPDPVLVHCIOQC 1500
DB 1674 GAVCSPCLVIPSPDPVWLPENITADTLEHMEPVKYQSICTGRORWHPDPVLVHCIOQC 1733
QY 1501 EPPQADGWCTTINNRAYCHYDGDCCSSTLSKKVLPFADCDLDECTGRPAEENQ 1558
DB 1734 EPPQADGWCTTINNRAYCHYDGDCCSSTLSKKVLPFADCDLDECTGRPAEENQ 1791

RESULT 2
US-09-827-998-3
; Sequence 3, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHWR-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 3
; LENGTH: 1791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-3

Query Match 99.8%; Score 8592; DB 9; Length 1791;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1555; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPPEBSONGEGSYREAEFTNSQVGLPILYFSGRREBRLLRPEVLAIEIPREAFVTEAWV 60
DB 234 SPPEBSONGEGSYREAEFTNSQVGLPILYFSGRREBRLLRPEVLAIEIPREAFVTEAWV 293
QY 61 KPEGGONNPALIIAGVFNCSHTVSDKGWALGIRSGKDGKRDARFFPSLCTDRVKKATIL 120
DB 294 KPEGGONNPALIIAGVFNCSHTVSDKGWALGIRSGKDGKRDARFFPSLCTDRVKKATIL 353
QY 121 ISHSRYOPGTWTHVAATYDGRHMAIYVDGTQVASSLDOSGPLNSPFMA5CRSLLGGDS 180
DB 354 ISHSRYOPGTWTHVAATYDGRHMAIYVDGTQVASSLDOSGPLNSPFMA5CRSLLGGDS 413
QY 181 EDGYFRGHGLTILVFWSTALPOSHFOHSSOHSGBEERATDLVLTASFEVNTWVPFRDE 240

```

414 EDGHYFRGHLGTLVFWSTALPQSHFQHSQHSSEEBATDLVLTASFEPVNTWMPFRDE 473
QY KYRPLEVTLQGFEPPELISPLQPLCGQTVCDNVELLSQYNGYMPLRSEKXIRQVYVNIC 300
Db KYRPLEVTLQGFEPPELISPLQPLCGQTVCDNVELLSQYNGYMPLRSEKXIRQVYVNIC 533
QY DDEGLNPVSEBQIRLOHEALNEAFSRYNISMOQSVHGVNSTLRHRVVLVNCESKXIGN 360
Db DDEGLNPVSEBQIRLOHEALNEAFSRYNISMOQSVHGVNSTLRHRVVLVNCESKXIGN 593
QY 361 DHCDPECEHPLTGYDGDGCRLOQRCYSWNRDGLCHVECNMMLDFDGDCCDQVADV 420
Db DHCDPECEHPLTGYDGDGCRLOQRCYSWNRDGLCHVECNMMLDFDGDCCDQVADV 653
QY 421 KTCDDPSPKRAYSVKELKALQUNSTHFNITVFASVREDLAGAATWPDQXAVYTHG 480
Db KTCDDPSPKRAYSVKELKALQUNSTHFNITVFASVREDLAGAATWPDQXAVYTHG 713
QY 481 GIVSPRAYGMPGHTDMIHVEGHVGLXHYFKGVSESESQNDPCKETVPSEMETGDLCAD 540
Db GIVSPRAYGMPGHTDMIHVEGHVGLXHYFKGVSESESQNDPCKETVPSEMETGDLCAD 773
QY 541 TAPTPKSELCEBEPSTDTGCTFRPGAPFTNYSYTDNCTDNFTPNQVARMHCYLDLV 600
Db TAPTPKSELCEBEPSTDTGCTFRPGAPFTNYSYTDNCTDNFTPNQVARMHCYLDLV 833
QY 601 YQOMTESRKPTPIPIPPMVICQTNKSLTIHMLPPISGVYVYRAGSGLGACTEBGTFRQY 660
Db YQOMTESRKPTPIPIPPMVICQTNKSLTIHMLPPISGVYVYRAGSGLGACTEBGTFRQY 893
QY 661 VHTSSRRVCDSSGYWTPPEEAVGPDPVDOCEPSLOAMSPEVNIYHMMWTPCPTBGSL 720
Db VHTSSRRVCDSSGYWTPPEEAVGPDPVDOCEPSLOAMSPEVNIYHMMWTPCPTBGSL 953
QY 721 ELLFQHPVQADTLTLMWTSFPMSSQVLFDTIELLENKESVHLGPLDTFCDIPLTIKLV 780
Db ELLFQHPVQADTLTLMWTSFPMSSQVLFDTIELLENKESVHLGPLDTFCDIPLTIKLV 1013
QY 781 DGKYSYKVTTFEDRIEIDALLTSOPHSPLCSGCRPVRYVULADPPASGLPVVYVTHSH 840
Db DGKYSYKVTTFEDRIEIDALLTSOPHSPLCSGCRPVRYVULADPPASGLPVVYVTHSH 1014
QY 841 RKPTDVEVTPGOMYOYVLAAGELGASPLNHNHGAAPVCGSGKYSERLGEBCDDGDL 900
Db RKPTDVEVTPGOMYOYVLAAGELGASPLNHNHGAAPVCGSGKYSERLGEBCDDGDL 1074
QY 901 VSGDGSKVCLEBEGFNCVGBPSLCYMYEGDGICEPERKTSIVDCGIYTPKGYLDQWAT 960
Db VSGDGSKVCLEBEGFNCVGBPSLCYMYEGDGICEPERKTSIVDCGIYTPKGYLDQWAT 1134
QY 961 RAYSHEDKXKCPVSLVTGERPHSLICTSYHAPDLFNHRPLTGWPCVASENETODRSBP 1020
Db RAYSHEDKXKCPVSLVTGERPHSLICTSYHAPDLFNHRPLTGWPCVASENETODRSBP 1194
QY 1021 EGSLSKXEDVWLKVCNRPGEARAIETFLTLDGLVPGHQOPTYVTLVTVDRGSNHSIGT 1080
Db EGSLSKXEDVWLKVCNRPGEARAIETFLTLDGLVPGHQOPTYVTLVTVDRGSNHSIGT 1254
QY 1081 YGSLSCQNPPLIINTVTHQNVLFHHTTSVLLNFSSPRVIGISAVALTSSRIGLSAPNSCIS 1140
Db YGSLSCQNPPLIINTVTHQNVLFHHTTSVLLNFSSPRVIGISAVALTSSRIGLSAPNSCIS 1314
QY 1141 EDEGQNHQOGSCIRPCGKODSCPSLLIDHADVNVCTSIGGLMKCAITCQGFALQASS 1200
Db EDEGQNHQOGSCIRPCGKODSCPSLLIDHADVNVCTSIGGLMKCAITCQGFALQASS 1374
QY 1201 GQYIRPQOKETLLTCSSGMDQNVSCLPVDCGVPDPSLVNANFSCSEBGTFLKRCISIC 1260
Db GQYIRPQOKETLLTCSSGMDQNVSCLPVDCGVPDPSLVNANFSCSEBGTFLKRCISIC 1434
QY 1261 VPPAKLOGLSFWLTCLEBDGLWSLPEVYCKLECDAPPIIILNANLLPCLQDNHVDGTCIK 1320
Db VPPAKLOGLSFWLTCLEBDGLWSLPEVYCKLECDAPPIIILNANLLPCLQDNHVDGTCIK 1494

QY 1321 YECKPGYVAESASAGKVRNKLTKIQCLEGGIWEQSGCIPVCEPPVPFEGMECTNGFS 1380
Db YECKPGYVAESASAGKVRNKLTKIQCLEGGIWEQSGCIPVCEPPVPFEGMECTNGFS 1613
QY 1381 LDSQCVLNCNOERREKLPICTKEGLMTQEFPLCENLQGECPPEPSLINSYEKCEQGYGI 1440
Db LDSQCVLNCNOERREKLPICTKEGLMTQEFPLCENLQGECPPEPSLINSYEKCEQGYGI 1673
QY 1441 GAVCSPLCVIIPSPDVMLENITADTLEHMEPVKVOSIVCTGRQWHPDPVLVHCIOQC 1500
Db GAVCSPLCVIIPSPDVMLENITADTLEHMEPVKVOSIVCTGRQWHPDPVLVHCIOQC 1733
QY 1501 EPPQADGCDTIINRAYCHVDGDCSSSTLSSKKVIFPADCDLDECTCRPKABENO 1558
Db EPPQADGCDTIINRAYCHVDGDCSSSTLSSKKVIFPADCDLDECTCRPKABENO 1791

RESULT 3
US-10-675-685-3
Sequence 3, Application US/10675685
Publication No. US20040063134A1
GENERAL INFORMATION:
APPLICANT: Shannon, Mark
TITLE OR INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: PR0114
CURRENT APPLICATION NUMBER: US/10/675,685
CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 3
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
US-10-675-685-3

Query Match 99.8%; Score 8592; DB 15; Length 1791;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 1555; Conservative 1; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPEESNONGEGSYREAEFTNSQVGLPIYFSGRRRLLRPEVLAIEPREAEFTVEAMV 60
Db 234 SPEESNONGEGSYREAEFTNSQVGLPIYFSGRRRLLRPEVLAIEPREAEFTVEAMV 293
QY 61 KPREGQNNPAIAGVPNCGSHVSDKGMALGIRGKDKGRDAFFPSLCTDRVYKATIL 120
Db 294 KPREGQNNPAIAGVPNCGSHVSDKGMALGIRGKDKGRDAFFPSLCTDRVYKATIL 353
QY 121 ISHSRYQPTWTHVAAATYDGRSHMALYVDGTQVASSLDSQSGPLNSPFMASSCRSLLLGSDS 180
Db 354 ISHSRYQPTWTHVAAATYDGRSHMALYVDGTQVASSLDSQSGPLNSPFMASSCRSLLLGSDS 413
QY 181 EDGHYFRGHLGTLVFWSTALPQSHFQHSQHSSEEBATDLVLTASFEPVNTWMPFRDE 240
Db 414 EDGHYFRGHLGTLVFWSTALPQSHFQHSQHSSEEBATDLVLTASFEPVNTWMPFRDE 473
QY 241 KYRPLEVTLQGFEPPELISPLQPLCGQTVCDNVELLSQYNGYMPLRSEKXIRQVYVNIC 300
Db 474 KYRPLEVTLQGFEPPELISPLQPLCGQTVCDNVELLSQYNGYMPLRSEKXIRQVYVNIC 533
QY 301 DDEGLNPVSEBQIRLOHEALNEAFSRYNISMOQSVHGVNSTLRHRVVLVNCESKXIGN 360
Db 534 DDEGLNPVSEBQIRLOHEALNEAFSRYNISMOQSVHGVNSTLRHRVVLVNCESKXIGN 593
QY 361 DHCDPECEHPLTGYDGDGCRLOQRCYSWNRDGLCHVECNMMLDFDGDCCDQVADV 420
Db 594 DHCDPECEHPLTGYDGDGCRLOQRCYSWNRDGLCHVECNMMLDFDGDCCDQVADV 653

421 KTCFDDSPKRAVMSVKEALKEALQLNSTHPLNIYFASVREDLAGATWMDKDAVTHLG 480
Db KTCFDDSPKRAVMSVKEALKEALQLNSTHPLNIYFASVREDLAGATWMDKDAVTHLG 713
QY 481 GIVLSPAYYGMPTHTMHEVGHVGLYHVFKGVSEBSCNDPCKETVPSMETGDLCAD 540
Db GIVLSPAYYGMPTHTMHEVGHVGLYHVFKGVSEBSCNDPCKETVPSMETGDLCAD 773
QY 541 TAPPKSELCREBEPTSDTCGTPRPGAFTNNVSYTDNCTDNTPNQVARMICYLDLV 600
Db TAPPKSELCREBEPTSDTCGTPRPGAFTNNVSYTDNCTDNTPNQVARMICYLDLV 833
QY 601 YQOMTESRKPPIPIPMVIGQTKSLTIHMLPISGVVYBRASGSLGCACTEBGTFRQY 660
Db YQOMTESRKPPIPIPMVIGQTKSLTIHMLPISGVVYBRASGSLGCACTEBGTFRQY 893
QY 661 VHTASSRRVCDSSGWTPEEAVGPPDVDPCEPSIQAMSPEVHLVHMNTVPCETEGCSL 720
Db VHTASSRRVCDSSGWTPEEAVGPPDVDPCEPSIQAMSPEVHLVHMNTVPCETEGCSL 953
QY 721 ELLFOHPVQADTTLTMTSFFMESQVLPDTEILLNKESVHLGPDTRCDIPLTIKLHV 780
Db ELLFOHPVQADTTLTMTSFFMESQVLPDTEILLNKESVHLGPDTRCDIPLTIKLHV 1013
QY 781 DGKYSGVVYTFDERIEIDALLTSQPHSPICSGCRPVRYOVLRDPPASGLPVVYTHSH 840
Db DGKYSGVVYTFDERIEIDALLTSQPHSPICSGCRPVRYOVLRDPPASGLPVVYTHSH 1073
QY 841 RKFTDVEVTPGQOMTOYOVLAAGBELGASPLNHIHAPYCGDGKVSERLGEBCDDGL 900
Db RKFTDVEVTPGQOMTOYOVLAAGBELGASPLNHIHAPYCGDGKVSERLGEBCDDGL 1133
QY 901 VSGGSCSVCELEGGENCVEBPSLCYMEBGDICEPERKTSIVDCGITYPKGLDQMAT 960
Db VSGGSCSVCELEGGENCVEBPSLCYMEBGDICEPERKTSIVDCGITYPKGLDQMAT 1193
QY 961 RAYSHEDKCKCPVSLVTGEPSHICTSYHPLDNHRLTGMFPCVASENETQDRSEOP 1020
Db RAYSHEDKCKCPVSLVTGEPSHICTSYHPLDNHRLTGMFPCVASENETQDRSEOP 1253
QY 1021 EGSLLKEDVWLKVCENRPGBARAIFPLTTDGLVPGHQOPTYVTLVLTVDVSGNSHLSGT 1080
Db EGSLLKEDVWLKVCENRPGBARAIFPLTTDGLVPGHQOPTYVTLVLTVDVSGNSHLSGT 1313
QY 1081 YGLSCQHNPLIINTHQNVLPHHTTSVLFNFSSPRVIGISAVALRTSRIGLSAPNSCIS 1140
Db YGLSCQHNPLIINTHQNVLPHHTTSVLFNFSSPRVIGISAVALRTSRIGLSAPNSCIS 1373
QY 1141 EDEGQNHQSGCIRPCKGKODSCPSLLLDHADVNTCSIGFLMKCAITCORGALQASS 1200
Db EDEGQNHQSGCIRPCKGKODSCPSLLLDHADVNTCSIGFLMKCAITCORGALQASS 1433
QY 1201 GQYIRPMQKELLITCSSGMDQONVCLPVDGVPDPISLVNYANFSCSEGTFLKRCISIC 1260
Db GQYIRPMQKELLITCSSGMDQONVCLPVDGVPDPISLVNYANFSCSEGTFLKRCISIC 1493
QY 1261 VPPAKLOGSLFWLTCLEBGLMSLEPVYCKLECDAPITLIANNLLPHCLDNHVGITICK 1320
Db VPPAKLOGSLFWLTCLEBGLMSLEPVYCKLECDAPITLIANNLLPHCLDNHVGITICK 1553
QY 1321 YECRPGYVVASAGKVRNKLKICQLEGGIMEQSCIPVCEPDPVPEFEGMECTNGFS 1380
Db YECRPGYVVASAGKVRNKLKICQLEGGIMEQSCIPVCEPDPVPEFEGMECTNGFS 1613
QY 1381 LDSQCVLNCQDEREKLPLCTKEGIMTQEFKLCENTLQCECPRPSSELSNVEYKCEQYGI 1440
Db LDSQCVLNCQDEREKLPLCTKEGIMTQEFKLCENTLQCECPRPSSELSNVEYKCEQYGI 1673
QY 1441 GAVSPLCLVPRSPVWMLPENITADTLBHMMEPVKVGSIYCTGRQWHPDPVLVHCTQSC 1500
Db GAVSPLCLVPRSPVWMLPENITADTLBHMMEPVKVGSIYCTGRQWHPDPVLVHCTQSC 1733
QY 1501 EPPQADGMCDTIINNRAYCHVDGDCSSSTLSKKVIFPADCDLDECTCRDPKAEHQ 1558

Db 1734 EPPQADGMCDTIINNRAYCHVDGDCSSSTLSKKVIFPADCDLDECTCRDPKAEHQ 1791

RESULT 4
US-09-983-10
; Sequence 10, Application US/09827998
; Patent No. US20020102252A1
GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHOF-8
CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aeonica Sequence Listing Engine
; SEQ ID NO 10
; LENGTH: 1770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-983-10

Query Match 95.9%; Score 8263; DB 9; Length 1770;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPPEBSONGSGSYBEAETFNQVGLPLIYFSGRBRLLRPEVLAETPREAFVYAWY 60
Db 234 SPPEBSONGSGSYBEAETFNQVGLPLIYFSGRBRLLRPEVLAETPREAFVYAWY 233
QY 61 KPBGQNNPAILIAGVFNCSHTVSDKGMALGIRSGDKGRDARFFSLCTDRVKKATIL 120
Db 294 KPBGQNNPAILIAGVFNCSHTVSDKGMALGIRSGDKGRDARFFSLCTDRVKKATIL 353
QY 121 ISHSRYQPTGTHVAATYDGRHMLVYDGTQVASSLDQSGPLNSPMAKCRSLLGSDS 180
Db 354 ISHSRYQPTGTHVAATYDGRHMLVYDGTQVASSLDQSGPLNSPMAKCRSLLGSDS 413
QY 181 EDGHYFRGHGTLVFNSTALPOSHFQSSQHSSEEBATDLVLTASFEPNTEWVPRDE 240
Db 414 EDGHYFRGHGTLVFNSTALPOSHFQSSQHSSEEBATDLVLTASFEPNTEWVPRDE 473
QY 241 KYPRLEVLQGFEBEPILSPLQPLCGQVCDNVELISQYNGYWPJRGEXVIRYQVYVNIC 300
Db 474 KYPRLEVLQGFEBEPILSPLQPLCGQVCDNVELISQYNGYWPJRGEXVIRYQVYVNIC 533
QY 301 DDEGLNPVSEQIRLOHEALNEAFSRYNISWQLSVHQNSTLRRVVLVNCSEPSKIGN 360
Db 534 DDEGLNPVSEQIRLOHEALNEAFSRYNISWQLSVHQNSTLRRVVLVNCSEPSKIGN 593
QY 361 DHCDBCEHPRLGYDGDGCRLOGRQCYSNRBDLCHVECNMMLNDDDDGCDPOVADVR 420
Db 594 DHCDBCEHPRLGYDGDGCRLOGRQCYSNRBDLCHVECNMMLNDDDDGCDPOVADVR 653
QY 421 KTCFDDSPKRAVMSVKEALKEALQLNSTHPLNIYFASVREDLAGATWMDKDAVTHLG 480
Db 481 KTCFDDSPKRAVMSVKEALKEALQLNSTHPLNIYFASVREDLAGATWMDKDAVTHLG 713
QY 714 GIVLSPAYYGMPTHTMHEVGHVGLYHVFKGVSEBSCNDPCKETVPSMETGDLCAD 540
Db 541 TAPPKSELCREBEPTSDTCGTPRPGAFTNNVSYTDNCTDNTPNQVARMICYLDLV 600
QY 601 YQOMTESRKPPIPIPMVIGQTKSLTIHMLPISGVVYBRASGSLGCACTEBGTFRQY 660
Db 774 TAPPKSELCREBEPTSDTCGTPRPGAFTNNVSYTDNCTDNTPNQVARMICYLDLV 833

834 YQWTSRKRPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLGACTEDGTFRQY 893
QY VHTASSRRVCDSSGWTPEBAVGPDPVDOCPCEPSLOAMSEBVHLIYHNMVTPCTEGCSL 720
Db VHTASSRRVCDSSGWTPEBAVGPDPVDOCPCEPSLOAMSEBVHLIYHNMVTPCTEGCSL 953
QY 721 ELLFQHPVQADTLTLMTWTSFPMESQVLFDTFELLLENKESVHLGPDLPFCOIPLTILKLV 780
Db 954 ELLFQHPVQADTLTLMTWTSFPMESQVLFDTFELLLENKESVHLGPDLPFCOIPLTILKLV 1013
QY 781 DGRVSGVKKVYTFDERIEIDALLTSQPHSPLCSGCRPRVYQVLRDPFASGLPVVYVTHSH 840
Db 1014 DGRVSGVKKVYTFDERIEIDALLTSQPHSPLCSGCRPRVYQVLRDPFASGLPVVYVTHSH 1073
QY 841 RKPFDVAVTTPQOMQYQVLAAGELGASPLNHIHGAIPVCGGKYSERIGEECDGDL 900
Db 1074 RKPFDVAVTTPQOMQYQVLAAGELGASPLNHIHGAIPVCGGKYSERIGEECDGDL 1133
QY 901 VSGDGSCKVCELEBGFNCVGPBPSLCYMYEGDICEPFRKTSIVDCGITYPKGYLDQWAT 960
Db 1134 VSGDGSCKVCELEBGFNCVGPBPSLCYMYEGDICEPFRKTSIVDCGITYPKGYLDQWAT 1193
QY 961 RAVSSHEDKKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETODRSBOP 1020
Db 1194 RAVSSHEDKKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETODRSBOP 1253
QY 1021 EGSJLKKDEWMLKVCNRPGEARAIFFLTDTGIVPGEHQPTVTLTYLTVRGSNHSIGT 1080
Db 1254 EGSJLKKDEWMLKVCNRPGEARAIFFLTDTGIVPGEHQPTVTLTYLTVRGSNHSIGT 1313
QY 1081 YGASCOHNPILINTHONVLFHHTSVLNFSSPRVIGISAVARTSRIGLSAPNSCIS 1140
Db 1314 YGASCOHNPILINTHONVLFHHTSVLNFSSPRVIGISAVARTSRIGLSAPNSCIS 1373
QY 1141 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNVCTSIGPGLMKCAITTCQRFALQASS 1200
Db 1374 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNVCTSIGPGLMKCAITTCQRFALQASS 1433
QY 1201 GQYIRPMQKELLTCCSSGHMDQNSCLPVDGVPDPSSLVNYANFSGEBTKFKLRCSISC 1260
Db 1434 GQYIRPMQKELLTCCSSGHMDQNSCLPVDGVPDPSSLVNYANFSGEBTKFKLRCSISC 1493
QY 1261 VPPAKLOGLSPMLTCLSDGLMSLPEVYCKLECDAPRIILANANILLPHCLDNDHVGITCK 1320
Db 1494 VPPAKLOGLSPMLTCLSDGLMSLPEVYCKLECDAPRIILANANILLPHCLDNDHVGITCK 1553
QY 1321 YECKRGYVAESAGKVRNKLKIQCLEGIMWQSGCIPVCEBPPPVFEGMECTNGFS 1380
Db 1554 YECKRGYVAESAGKVRNKLKIQCLEGIMWQSGCIPVCEBPPPVFEGMECTNGFS 1613
QY 1381 LDSQCVLNCQERKLPILCTKEGLMTQEFKLCENLQCECPRPBSLNSVEYKCEQYGI 1440
Db 1614 LDSQCVLNCQERKLPILCTKEGLMTQEFKLCENLQCECPRPBSLNSVEYKCEQYGI 1673
QY 1441 GAVCSPLCVIPSPDPMVLPENITADTLEHMMERPKVQSIYCTGRQNHPRVVLHNCIQSC 1500
Db 1674 GAVCSPLCVIPSPDPMVLPENITADTLEHMMERPKVQSIYCTGRQNHPRVVLHNCIQSC 1733
QY 1501 E 1501
Db 1734 E 1734

RESULT 5
US-10-675-685-10
; Sequence 10, Application US/10675685
; Publication No. US20040063134A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yichong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: P00114
; CURRENT APPLICATION NUMBER: US/10/675, 685

CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aeonica Sequence Listing Engine
SEQ ID NO 10
LENGTH: 1770
TYPE: PRT
ORGANISM: Homo sapiens
US-10-675-685-10

Query Match 95.9%; Score 8263; DB 15; Length 1770;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 SPPESSNQNGEGSYREAFETFNQVGLPIIFYSGRRRLLRPREVLAIPEAFVTEAMV 60
Db 234 SPPESSNQNGEGSYREAFETFNQVGLPIIFYSGRRRLLRPREVLAIPEAFVTEAMV 293
QY 61 KPEGGQNNPAIAGVFNCSHTVSDKGMALGIRGDKGRDARFPFSLCTDRVYKATIL 120
Db 294 KPEGGQNNPAIAGVFNCSHTVSDKGMALGIRGDKGRDARFPFSLCTDRVYKATIL 353
QY 121 ISHSRYPGTWTHVATYDGRHMLYDGTQVASSLDQSGPLNSPFMAKCSLLGDS 180
Db 354 ISHSRYPGTWTHVATYDGRHMLYDGTQVASSLDQSGPLNSPFMAKCSLLGDS 413
QY 181 EDGHYFRGHGLTVFNWSTALPQSHFQSSQSSGSEETALDVLTFASPEPVTEWVPRDE 240
Db 414 EDGHYFRGHGLTVFNWSTALPQSHFQSSQSSGSEETALDVLTFASPEPVTEWVPRDE 473
QY 241 KYPRLEVLQGFEBEPELISLPQEPICQTVCDNELISQYNGVPLRGEKVIYQVYVNIC 300
Db 474 KYPRLEVLQGFEBEPELISLPQEPICQTVCDNELISQYNGVPLRGEKVIYQVYVNIC 533
QY 301 DDEGLNPIVSEBQIRLOHEALNEAFRNYNSKQLSHYQVNSTLRHVVLVNCPSKIGN 360
Db 534 DDEGLNPIVSEBQIRLOHEALNEAFRNYNSKQLSHYQVNSTLRHVVLVNCPSKIGN 593
QY 361 DHCDECEHPPLTGDGDCRLQGRCYSMNRDGLCHYECNNMLDPDGDCCDQVADV 420
Db 594 DHCDECEHPPLTGDGDCRLQGRCYSMNRDGLCHYECNNMLDPDGDCCDQVADV 653
QY 421 KTCFDPDSPRAYMSVKELEALQNSTHPLNTIYFASVREDLAAGATWPMXDVAVTHLG 480
Db 654 KTCFDPDSPRAYMSVKELEALQNSTHPLNTIYFASVREDLAAGATWPMXDVAVTHLG 713
QY 481 GIVLSPAYYGMFGHTDTMHEVGHVGLYHVFQVSRRESNDPCKETVPSMETGDLCAD 540
Db 714 GIVLSPAYYGMFGHTDTMHEVGHVGLYHVFQVSRRESNDPCKETVPSMETGDLCAD 773
QY 541 TAPTPKSELCREPEPSDTCGTRFPGAPFTNMSYTDNCTDFTNQVARNHCYLDLV 600
Db 774 TAPTPKSELCREPEPSDTCGTRFPGAPFTNMSYTDNCTDFTNQVARNHCYLDLV 833
QY 601 YQWTSRKRPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLGACTEDGTFRQY 660
Db 834 YQWTSRKRPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLGACTEDGTFRQY 893
QY 661 VHTASSRRVCDSSGWTPEBAVGPDPVDOCPCEPSLOAMSEBVHLIYHNMVTPCTEGCSL 720
Db 894 VHTASSRRVCDSSGWTPEBAVGPDPVDOCPCEPSLOAMSEBVHLIYHNMVTPCTEGCSL 953
QY 721 ELLFQHPVQADTLTLMTWTSFPMESQVLFDTFELLLENKESVHLGPDLPFCOIPLTILKLV 780
Db 954 ELLFQHPVQADTLTLMTWTSFPMESQVLFDTFELLLENKESVHLGPDLPFCOIPLTILKLV 1013
QY 781 DGRVSGVKKVYTFDERIEIDALLTSQPHSPLCSGCRPRVYQVLRDPFASGLPVVYVTHSH 840
Db 1014 DGRVSGVKKVYTFDERIEIDALLTSQPHSPLCSGCRPRVYQVLRDPFASGLPVVYVTHSH 1073

QY	841	KKFTDVEYTPCOMQYOYQVLAAGHGLGASAPPLNHIHGAIPVCGDKUSERI,GBECDDGDL	900
Db	1074	KKFTDVEYTPCOMQYOYQVLAAGHGLGASAPPLNHIHGAIPVCGDKUSERI,GBECDDGDL	1133
QY	901	VSGGGSKVCELEBGFNCVGEPSLTCYMEEGDGI CEPPFKRTIS IYDCGJLYTPKGYLDQMAT	960
Db	1134	VSGGGSKVCELEBGFNCVGEPSLTCYMEEGDGI CEPPFKRTIS IYDCGJLYTPKGYLDQMAT	1193
QY	961	RAYSHEDKTKCPVSLVTGEBPHSLI CTISYHPDL PNHRLTGMFPCVASENETODDRSEOP	1020
Db	1194	RAYSHEDKTKCPVSLVTGEBPHSLI CTISYHPDL PNHRLTGMFPCVASENETODDRSEOP	1253
QY	1021	EGSLKKEDEWMLKVCFPNPGEARAFIFLITTDGLVGEHOOPTWTL,YLTDVRSNHSJGT	1080
Db	1254	EGSLKKEDEWMLKVCFPNPGEARAFIFLITTDGLVGEHOOPTWTL,YLTDVRSNHSJGT	1313
QY	1081	YGLSCOHNP,LIJNVTHQONVL,FHHTTSLYLNFSSPRVGISAVALT,RTSSRIG,ISAPNSCIS	1140
Db	1314	YGLSCOHNP,LIJNVTHQONVL,FHHTTSLYLNFSSPRVGISAVALT,RTSSRIG,ISAPNSCIS	1373
QY	1141	EDEGONHGGOSCIRHPCCGKODSCPSLLLDHADVNNCTISIGGIMKCAITTCORGPLQASS	1200
Db	1374	EDEGONHGGOSCIRHPCCGKODSCPSLLLDHADVNNCTISIGGIMKCAITTCORGPLQASS	1433
QY	1201	GOYIRPMQKEILITSSSGHMDQNVCL,PVDCGVPPSLVNYANFSCSEGT,FKLRCSJSC	1260
Db	1434	GOYIRPMQKEILITSSSGHMDQNVCL,PVDCGVPPSLVNYANFSCSEGT,FKLRCSJSC	1493
QY	1261	VPPAKLQGLSPMLTCLBDGLMSLPEVYCKLBCDAP,PIILNANLLPHCLQDNHDVGT,CK	1320
Db	1494	VPPAKLQGLSPMLTCLBDGLMSLPEVYCKLBCDAP,PIILNANLLPHCLQDNHDVGT,CK	1553
QY	1321	YECRGGYVVASABEKVANKL,KTIOCLSGGI,MEGOSCI,PVYCEPP,PPVFEGBYE,ECTNFS	1380
Db	1554	YECRGGYVVASABEKVANKL,KTIOCLSGGI,MEGOSCI,PVYCEPP,PPVFEGBYE,ECTNFS	1613
QY	1381	LDSQCVLNCNBEREKL,PIILCTKEGLMTOEF,KLCENL,OGECBPP,SEBLSN,VEYKCEQGYGI	1440
Db	1614	LDSQCVLNCNBEREKL,PIILCTKEGLMTOEF,KLCENL,OGECBPP,SEBLSN,VEYKCEQGYGI	1673
QY	1441	GAVCSPLCVIIPSPDVM,IPENITADTLEHNM,EPVAVGSI,VTCTGRROHMPDPVLVHCIO,SC	1500
Db	1674	GAVCSPLCVIIPSPDVM,IPENITADTLEHNM,EPVAVGSI,VTCTGRROHMPDPVLVHCIO,SC	1733
QY	1501 E 1501		
Db	1734 E 1734		
RESULT 6			
US-09-827-998-16			
: Sequence 16, Application US/09827998			
: Patent No. US2002010252A1			
: GENERAL INFORMATION:			
: APPLICANT: Gu, Yizhong			
: APPLICANT: Shannon, Mark			
: TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E			
: FILE REFERENCE: MDWOPF-8			
: CURRENT APPLICATION NUMBER: US/09/827,998			
: CURRENT FILING DATE: 2001-04-06			
: PRIOR APPLICATION NUMBER: US 60/207,456			
: PRIOR FILING DATE: 2000-05-26			
: PRIOR APPLICATION NUMBER: US 60/236,359			
: PRIOR FILING DATE: 2000-09-27			
: NUMBER OF SEQ ID NOS: 1881			
: SOFTWARE: Aeomica Sequence Listing Engine			
: SEQ ID NO 16			
: LENGTH: 1385			
: TYPE: PRT			
: ORGANISM: Homo sapiens			
US-09-827-998-16			

Best Local Similarity 73.6%; Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 5; Indels 406; Gaps 1.

QY	I	SPBESNONGEGSYREAEFTNSQVGLPILYFSRRRLRLRPVLAEIPREATTWAMV	60
Db	234	SPBESNONGEGSYREAEFTNSQVGLPILYFSRRRLRLRPVLAEIPREATTWAMV	293
QY	61	KPEGONNPALIAVFDNCSHTVSDKGMALGIRSGDKGRDAFFPFLCTDRVKKATIL	120
Db	294	KPEGONNPALIA-----	306
QY	121	ISHSRYPGTWTHAATYDGRHMALYVDQTQVASSLDQSGPLNSPFMAACRSLLLGDS	180
Db	307	-----	306
QY	181	EDGHYFRGHLCTLYFWSTALPQSHFQHSQHSSEBEATDLVLTAASEPNTEWVPRDE	240
Db	307	-----	306
QY	241	KYPLBVLQGEPEPEILSLQPLQCGQTVCDNVELISQYNGWYPLRGEKIVRQVNNIC	300
Db	307	-----	306
QY	301	DDEGLNPVSEBQIRLOHEALNEAFSRXNYSWOLSVHQVHNSTLRHRVVLVNCPSKIGN	360
Db	307	-----	306
QY	361	DHCDBECHPLTGYDGDGDLQRCGYCSWMNRDGLCHYECNNMLNDPDDGCCDDQVADVR	420
Db	307	-----	306
QY	421	KTCFDPDSPKAYMSVKELKEALQLNSTHFLNIYFASSVREDLAATPMDKDAVTHLG	480
Db	307	-----G 307	307
QY	481	GIVLSPAYYMPGHTDTMHEVGVGLYHVKGVSSRESNDCCKETVBSMETGDLCAD	540
Db	308	GIVLSPAYYMPGHTDTMHEVGVGLYHVKGVSSRESNDCCKETVBSMETGDLCAD	367
QY	541	TAPLPKSLCEBPEPTSDTCFTFPFGAPFNVMNSYTDNDCTDNFTNOVARMHCYDLV	600
Db	368	TAPLPKSELCEBPEPTSDTCFTFPFGAPFNVMNSYTDNDCTDNFTNOVARMHCYDLV	427
QY	601	YQOMTESKRPPIPIIPMWIGQTNKSLTIHMLPISGVYVDRAAGSLCGACTBEGTFRQY	660
Db	428	YQOMTESKRPPIPIIPMWIGQTNKSLTIHMLPISGVYVDRAAGSLCGACTBEGTFRQY	487
QY	661	VHTASSRRVCSGSGYTPBEAVGPDDVQPCPSLQAWSPEVHL YHMMNTVPCBTEGCSL	720
Db	488	VHTASSRRVCSGSGYTPBEAVGPDDVQPCPSLQAWSPEVHL YHMMNTVPCBTEGCSL	547
QY	721	ELLFQHPQADTLLMTWTSFPMESSQVLPDTEILLENKESVHLGRLDPTFCDIPLTIKLV	780
Db	548	ELLFQHPQADTLLMTWTSFPMESSQVLPDTEILLENKESVHLGRLDPTFCDIPLTIKLV	607
QY	781	DGXVSGVUYVTFDERIEIDALLLSOPSPLCSGCRPVRYOVLDPFPASGLPVVYTHSH	840
Db	608	DGXVSGVUYVTFDERIEIDALLLSOPSPLCSGCRPVRYOVLDPFPASGLPVVYTHSH	667
QY	841	RKFTDVEVTPGOMYQOVLAEAGELGASPLNHHIGAPYCGDGXVSERLGBECDDGL	900
Db	668	RKFTDVEVTPGOMYQOVLAEAGELGASPLNHHIGAPYCGDGXVSERLGBECDDGL	727
QY	901	VSGDGSXVCELBEGFNCVGPSPSLCYATEEGGICEBPFRKTSYVDCGYTPKGYLDQWAT	960
Db	728	VSGDGSXVCELBEGFNCVGPSPSLCYATEEGGICEBPFRKTSYVDCGYTPKGYLDQWAT	787
QY	961	RAYSHHEKCKCPSLVLTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENTOODRSQOP	1020
Db	788	RAYSHHEKCKCPSLVLTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENTOODRSQOP	847
QY	1021	EGSLKEDEVALKYCFNRGEGARALFIPLTTDGLVPGEHQDPVTVL YLTDVRGSNNHSLGT	1080

Db 848 EGSLLKKEDEWMLKVCFNRRGEBARAIFILTTDGLVPEHQOPTYTLVLTDRGSHSISGT 907
Qy 1081 YGLSCQHNPLIINTTHQNVLPFHRTTSVLLNFPSSPRVGISAVALTSSRIGLSAPNSCIS 1140
Db 908 YGLSCQHNPLIINTTHQNVLPFHRTTSVLLNFPSSPRVGISAVALTSSRIGLSAPNSCIS 967
Qy 1141 EDEQNHQOGSCIHRRPGKODSCBSLLDHDVNVCTSIGPLMKCATTCORGFALQASS 1200
Db 968 EDEQNHQOGSCIHRRPGKODSCBSLLDHDVNVCTSIGPLMKCATTCORGFALQASS 1027
Qy 1201 GQYIRPMQKEILLTCSSGHDQNVSCLPVDCGVPDPSPILVNYANFSCSEGTFLKRCISIC 1260
Db 1028 EQYIRLMQKEILLTCSSGHDQNVSCLPVDCGVPDPSPILVNYANFSCSEGTFLKRCISIC 1087
Qy 1261 VPPAKLOGLSPWLTCLDEGLMSLPBVYCKEBCDAPITILNANLLPHCLQDNHDVTIC 1320
Db 1088 VPPAKLOGLSPWLTCLDEGLMSLPBVYCKEBCDAPITILNANLLPHCLQDNHDVTIC 1147
Qy 1321 YECKRGYVVAESAGKVNKLKXIOCLEGGIMEQSSCPVYCEPPRPVFEEMTECTNGFS 1380
Db 1148 YECKRGYVVAESAGKVNKLKXIOCLEGGIMEQSSCPVYCEPPRPVFEEMTECTNGFS 1207
Qy 1381 LDSQCVLNCQBERKLPILCTKEGLMTQEFKLCENTLOGECPPEPSSELSVEYKCEQGYGI 1440
Db 1208 LDSQCVLNCQBERKLPILCTKEGLMTQEFKLCENTLOGECPPEPSSELSVEYKCEQGYGI 1267
Qy 1441 GAVCSPLCVIPSPDPMVLPENITADTLEHMEPVKQSVICTGRQMHDPVLVHCIOQC 1500
Db 1268 GAVCSPLCVIPSPDPMVLPENITADTLEHMEPVKQSVICTGRQMHDPVLVHCIOQC 1327
Qy 1501 EPPQADMCOTINRRAYCHYDGCSCSTSSKVIIPPAADCDLDECTCRPKABENO 1558
Db 1328 EPPQADMCOTINRRAYCHYDGCSCSTSSKVIIPPAADCDLDECTCRPKABENO 1385

RESULT 7

US-10-675-685-16

Sequence 16, Application US/10675685
Publication No. US20040063134A1

GENERAL INFORMATION:

APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

FILE REFERENCE: P00114

CURRENT APPLICATION NUMBER: US/10/675, 685

CURRENT FILING DATE: 2003-09-30

PRIOR APPLICATION NUMBER: US 60/207,456

PRIOR FILING DATE: 2000-05-26

PRIOR APPLICATION NUMBER: US 60/236,359

PRIOR FILING DATE: 2000-09-27

NUMBER OF SEQ ID NOS: 1881

SOFTWARE: Aeomica Sequence Listing Engine

SEQ ID NO 16

LENGTH: 1385

TYPE: PRT

ORGANISM: Homo sapiens

US-10-675-685-16

Query Match 71.1%, Score 6126; DB 15; Length 1385;
Best Local Similarity 73.6%, Pred. No. 0;
Matches 1147; Conservative 0; Mismatches 5; Indels 406; Gaps 1;

Qy 1 SPPEESNQNGEGSYREAEFTNSQVGLPIILYFSGRRELLLRPVLAIEPREAEFTAVMW 60
Db 234 SPPEESNQNGEGSYREAEFTNSQVGLPIILYFSGRRELLLRPVLAIEPREAEFTAVMW 293
Qy 61 KPREGQNNPALIAVFNQCSHTVSDKMGALGIRSGKQKGRDAPFSLCTDRVKKATIL 120
Db 294 KPREGQNNPALIAVFNQCSHTVSDKMGALGIRSGKQKGRDAPFSLCTDRVKKATIL 306
Qy 121 ISHSRYQPGTWTHTAATYDGRHMAIYVDGTQVASSLDQSGPLNSPFMASCRSLLLGDS 180
Db 307 ISHSRYQPGTWTHTAATYDGRHMAIYVDGTQVASSLDQSGPLNSPFMASCRSLLLGDS 306

Qy 181 EDGHYFRGHGLCTLVFWSTALPQSHFQNSQHSCEBEATDLVLTASFEPPVNTWPPRDE 240
Db 307 -----
Qy 241 KYRPLEVLQGFEPPELILPLQPPLCQGTVCNDVLELSQVNGVWPLRGEKVIROYVNIC 300
Db 307 -----
Qy 301 DDEGLNPIVSEBQIRLOHEALNEAFSRYNISWQLSVQVHNSTLRHVRVLVNCPEPSKIGN 360
Db 307 -----
Qy 361 DHCDPECHPLTYGDGDCLQGRCYSMNRDGLCHVECNMMLNDFDDGCCDPQVADVR 420
Db 307 -----
Qy 421 KTCFDPSPKRYANVSEKLEALQJNSTHPLNTIFASSVREDLAGAATWPDKDAVTHLG 480
Db 307 -----
Qy 481 GIVLSPAYGMPGHTDMIHVGHVGLYHVFKVSRESQNDPCKETVPSEMETGDLCAD 540
Db 308 GIVLSPAYGMPGHTDMIHVGHVGLYHVFKVSRESQNDPCKETVPSEMETGDLCAD 367
Qy 541 TAPPKSELCREPEPSTDCGFTFPGAPFTNYSYTDNCTDNFTPNQVARMHCYLDLV 600
Db 368 TAPPKSELCREPEPSTDCGFTFPGAPFTNYSYTDNCTDNFTPNQVARMHCYLDLV 427
Qy 601 YQWTEBKRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYURAGSLCGACTEGCTROY 660
Db 428 YQWTEBKRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYURAGSLCGACTEGCTROY 487
Qy 661 VHTASSRVCDSQSGYMTPEEAVGPDPDQCEPBLQJMSPEVHLYHMMTVPCPTBEGSL 720
Db 488 VHTASSRVCDSQSGYMTPEEAVGPDPDQCEPBLQJMSPEVHLYHMMTVPCPTBEGSL 547
Qy 721 ELTFQHPVQADTLTLMWTSFPMSSQVLPTEILLNKESVHLGDLPTFCDIPLTIKLV 780
Db 548 ELTFQHPVQADTLTLMWTSFPMSSQVLPTEILLNKESVHLGDLPTFCDIPLTIKLV 607
Qy 781 DGKVSQVYVTFPDERIEDAALLTSOPHSPICSGCRVRYOVLADPPASGLPVVVHSH 840
Db 608 DGKVSQVYVTFPDERIEDAALLTSOPHSPICSGCRVRYOVLADPPASGLPVVVHSH 667
Qy 841 RKFTDVEVTPQOMQYOVYLAAGELGEASPLNHIHICAPYCGDGKYSERLGEBCDDGL 900
Db 668 RKFTDVEVTPQOMQYOVYLAAGELGEASPLNHIHICAPYCGDGKYSERLGEBCDDGL 727
Qy 901 VSGDGSKVCLEBEGFNCVGEPSLCYMYEGDICEPERKTSIVDCGIYTPKGYLDQWAT 960
Db 728 VSGDGSKVCLEBEGFNCVGEPSLCYMYEGDICEPERKTSIVDCGIYTPKGYLDQWAT 787
Qy 961 RAYSHEDKKKCPVSLVTGEPHSLICTSYHPLDNHPLTCGMPCVASENETODRSEOP 1020
Db 788 RAYSHEDKKKCPVSLVTGEPHSLICTSYHPLDNHPLTCGMPCVASENETODRSEOP 847
Qy 1021 EGSLLKKEDEWMLKVCFNRRGEBARAIFILTTDGLVPEHQOPTYTLVLTDRGSHSISGT 1080
Db 848 EGSLLKKEDEWMLKVCFNRRGEBARAIFILTTDGLVPEHQOPTYTLVLTDRGSHSISGT 907
Qy 1081 YGLSCQHNPLIINTTHQNVLPFHRTTSVLLNFPSSPRVGISAVALTSSRIGLSAPNSCIS 1140
Db 908 YGLSCQHNPLIINTTHQNVLPFHRTTSVLLNFPSSPRVGISAVALTSSRIGLSAPNSCIS 967
Qy 1141 EDEQNHQOGSCIHRRPGKODSCBSLLDHDVNVCTSIGPLMKCATTCORGFALQASS 1200
Db 968 EDEQNHQOGSCIHRRPGKODSCBSLLDHDVNVCTSIGPLMKCATTCORGFALQASS 1027
Qy 1201 GQYIRPMQKEILLTCSSGHDQNVSCLPVDCGVPDPSPILVNYANFSCSEGTFLKRCISIC 1260
Db 1028 EQYIRLMQKEILLTCSSGHDQNVSCLPVDCGVPDPSPILVNYANFSCSEGTFLKRCISIC 1087

Qy	1261	VPRKLTQSLSMWLTCTLEBGLMSLPEVYCKEBCDPAPTILNANLLPHCLQDNHVGITCK	1320
Dp	1088	VPRKLTQSLSMWLTCTLEBGLMSLPEVYCKEBCDPAPTILNANLLPHCLQDNHVGITCK	1147
Qy	1321	YECKRGYYVAASAGKVNKLKLTQCTLEGGIMEQSCIPVCEPPRPVFEQMYECTNGFS	1380
Dp	1148	YECKRGYYVAASAGKVNKLKLTQCTLEGGIMEQSCIPVCEPPRPVFEQMYECTNGFS	1207
Qy	1381	LDSCVTLNCNOREKLTPLTCTKEGIMTQEPFLCENLQSECPRPSELSNVYKCEQGYGI	1440
Dp	1208	LDSCVTLNCNOREKLTPLTCTKEGIMTQEPFLCENLQSECPRPSELSNVYKCEQGYGI	1267
Qy	1441	GAVCSPLCVIPSDPVMLENITADTLTEHMEPVKVGSICTGRQWHPDEVLVHCIOSC	1500
Dp	1268	GAVCSPLCVIPSDPVMLENITADTLTEHMEPVKVGSICTGRQWHPDEVLVHCIOSC	1327
Qy	1501	EPQADGDCDITINNRAYCHYDGGCCSSTLSKVTIPRAACDDIDECRCRPAKEENO	1558
Dp	1328	EPQADGDCDITINNRAYCHYDGGCCSSTLSKVTIPRAACDDIDECRCRPAKEENO	1385

RESULT 8
US-09-983-025-25

```

APPLICANT: OXVIG, Claus
APPLICANT: OVERGAARD, Michael T.
TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAPP-A2)
FILE REFERENCE: OXVIG=1A
CURRENT APPLICATION NUMBER: US/09/983,025
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/241,840
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: DK PA 2000 01571
PRIOR FILING DATE: 2000-10-20
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1.1
SEQ ID NO 25
LENGTH: 1627
TYPE: PR1
ORGANISM: Homo sapiens
US-09-983-025-25

Query Match      45.5%; Score 3916.5; DB 10; Length 1627;
Best Local Similarity 45.8%; Pred. No. 8.8e-297;
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

QY    16 REATFNFSQVGLP--LYFSGRRRLR--LREVLAEIPREAFTYEAWKPKPGGNNPALI 72
      ||| : | | | | | | | | | | | | | | : | | : | | | | | | | | |
DB    80 REAGCAATEEPSPRALYPFGSRGEQLRLRADL--ELPRDAFTYLQWLRAGAAGGRSPVI 137
QY    73 AGVDNCSSHUTSDGMALGIRSGDKGRDARPFPSLCTDDVKKATILISHRYOPGTWT 132
      ::| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB    138 TGLYDKCSYISRDKGVVGHITISDQNKDRPYFFSLKTIDARQYTINARSTLPQWV 197
QY    133 HVAATYDGRHVALYVDTGVASLSLDQSGPLNSPFMASCRSILLGDSSSEDPHYERHLGT 192
      :||| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
DB    198 YLAATYDQGFVKLYVNGAQVATSGEQVGIFSPILTQCKKVLMLG--SALHNRYGIETH 255
QY    193 LVFWSTALPQSHFOHSQSSHGSEBAIDLVTLASFEPNPTWVPFRDEKYTRLEV--LQG 250
      :| : | : | : | : | : | : | : | : | : | : | : | : | : | : |
DB    256 FSLMKVARTQRELLSDMETHGNATLPOLLLOEWMDNVKHAMSPMKOGSSPKVEFSNAG 315
QY    251 FEPEPELLSPROPICGGTVCNDVELTSQVNGWMPRLGEKEYTRYOVNICODEGLNPVS 310
      : : | : | | | | | | | | | | : | : | : | : | : | : | : | : |
DB    316 FLFD----TSLPEPLCGQTLCDNTEVLASTNQLSFPQPKVVRKRIVNALVEDHKNPVT 371
QY    311 EEQRIOLHEALNEAFNRYNISWQSIVHQVNSTLRHRVVLVNCEPSKIGNDHCDPECBP 370
      :| : | | | | | | | | | | : | : | : | : | : | : | : | : | : |
DB    372 REQVDYDFQHQLAEAFKOYNISMELDYLEVSNSSLRRLRIILANCOISKIGDCNCPENCHT 431
QY    371 LTGYDGDCR-LQGRCYSMNRBDGLCHVECNMLNDFPDGDCDPQAVARKTCFDPDSP 429

```

```

Db 432 LTGHDDGDCHRLHRAPVKKQHNGVCDMDNRYERNFNDGGECDDPELTIVTQCFDPDSP 491
Qy 430 KRAYMSYKELKEALQJNSTHFLNITYPASSVREDLAGAATYPMIDKDAVTHLGGIVLSPAY 489
Db 492 HRAVLIVNELKNIKJLKDGSHTLNIFFPKSSSEEBELAGVATPMWKEALMHJGGIVLWSPY 551
Qy 490 GMRHDTDTMHVENVHVLGLYHVFKGVSEERSCDNPKCEVYPSMETGDLCAVDTPTKSEL 549
Db 552 GMPGHHTMHMEIGHSHLGLYHVFEGISEIOSCDPMCEBPSSEBTGDLCDNTNPAHPGHS 611
Qy 550 CREBPTSDTCGFPRFGAPFTYVMSYTDNDCTDNFNPNOVAMHCLDLVYOOWTESRK 609
Db 612 CGDGGPNDTCGFHSFNTYRNNFMSYADDCTDSFTPNQVAMHCLDLVYOGMQRK 671
Qy 610 PTPPIRPMVIGQTNKSLTIHMLRPIISGVVYDRASSLCAACTEDGTFRQYVHTASSRV 669
Db 672 PAPVALAPQVLGHTTDSVTLEWFPPIDGHPFERBELSACHLCEGRILVQYASNASSPMP 731
Qy 670 CDSSGYTPREAVRPPVDQPCERSLOANRPEVHLIMNTVQCP--TEGSLLELPHQV 728
Db 732 CSPGSHMSPREABHPVBEQPCSSVATVMSPNASVNPHTVPACPEBOGGYLELEPIYPL 791
Qy 729 QADTLTLMVT--SEFMSSQVLPFTBLTENKESVHLGPIDFTCDIPLATKL-HVDGKVS 785
Db 792 VPESLTIWTFVSTIDMSSGAVNDIKLLAVSGKISLIGPQNVCDVPLTIRLMDVGEHY 851
Qy 786 GKVYTFDERLEIDALLTSQPHSPLCSGCRPVRYOVLARPPASGLPVVVTSHSRFTD 845
Db 852 GIQIYTLDEHLEIDAMLTSTADPTLCLOKPKLYKVKVDRPPLQMDVASIL-HLNRKFVD 910
Qy 846 VEVTPGQMYQVYLAEGSELGERSPLNIIHAPYGGDKVSEBRJGEECDODDLYSGDG 905
Db 911 MDLMIGSYQVWYVTTISGTESESPAVYTIHKGVCGDGI1OKDDQEBQCDNMKNKNDG 970
Qy 906 CSKYCELSEEGNCGVGEBSLCMYEGDICEPFEKRTS1VDCGIYTPKGYDQMATRAYSS 965
Db 971 CSLCRQGVSNFNCIDERSRCYFHDDGVCEFEKRTS1KDCGYTTPOGFLDQMAASNAVS 1030
Qy 966 HEDKKKCPVSLVTGP-HSLICTSYHDDLPHNRPLTGMFPCVASENETODRSEBQREGSL 1024
Db 1031 HQD-QQCPGMVYIIGQPAASQVCRKTVIDLSEGISQHAMVYCTTISYFVSQ----- 1078
Qy 1025 KKEBEWMLKYCFNRPGSARAF1FLFTLDGLVBEHQRPVYTLVLYTVRGSNHSJLGYGLS 1084
Db 1079 LAQTFPLIRAYFSQPMVAAVIYHLYVDGYTDQOKETISVGLDLPTKQSHDLGHLVLS 1138
Qy 1085 CQHPHLLIINTYHQNVLFFHTTSVLINFSFPRVIGISVVALRTSSRIGLSAPNSCISEDEG 1144
Db 1139 CRNNPPLLIPVNHDISQPFYHSQAVRVSFSSPLVAISGALRSDNDPDTVLSSC-QRGEL 1197
Qy 1145 QNHOGSCIRHPCCKODSCPSLILDLHADVYNCTSI-----GPGLMKCAITCORFALQASS 1200
Db 1198 YSPRAGQCVHAGACKTD-CPELAVENAS-LNCSSSDRYHG---AQCTVSCRTGYVLQIR 1252
Qy 1201 GQYIRPMQ--KEIILTCSSGHMDONVSLFVDCGVDPDSLIVNTANFSCSGTGFLLKRCST 1258
Db 1253 DDELIRKQGTGSVYVLTCEBKMKKQVACBFDVCSIPDHQVUYAASFSCREGTTFGSCSF 1312
Qy 1259 SCVPRALQGISPMVLTCELDGKMSLPBVYCKECDAPRIILNANLILPHLODNHDTGI 1318
Db 1313 QCRHPADQKGNNSLITWEMEDGLMSFPALCELMCLAPRPANADLQIARCREKNHKKVSF 1372
Qy 1319 CKYCEKGGYVYAESAEGKVENKLLKIQCELGAGIWEQSCIPVCEPBPVPEGYETECG 1378
Db 1373 CKYCKKGGHYVPGSSR-KSKKRAFKQCTODDGSQMOBACVPLVCDPPPRKPHGLGYCTNG 1431
Qy 1379 FSLDSQCVLNC-----NQBERKPLICTKEGLWTOEFKLCENTIOGCEBPPPSLNG-VEX 1432
Db 1432 FQFNSBCKIKCEDSDAQGLGSNVYIHCRRKDGTVNGSFHYVOEMQGCQ--SVYNEJLNSYTKL 1490
Qy 1433 KCBOGYGIGAVCSLCTYIPSPDPMLEPNTADTLEHMEPVAVQVSIYCTGRGROWHPDPV 1492

```


Db 1491 QCPDGAIGSBGATSCDHNSESIILPMNVTRDIPLMLNPRYERVVCTAGLKMYPHBA 1550
Qy 1493 LVHCLQSEFPQADGWCCTTNNRAYCHVDGDCSSTLSSKKVLPFAADCLD-ECTORD 1551
Db 1551 LHHGVCGEPEPMGNDYCDALNNRAFCNVDGDCCTSTVTKTKVLPFPMSCDLQGDGACARD 1610
Qy 1552 PKAEN 1557
Db 1611 PQAQEH 1616

RESULT 9
US-10-295-027-663
Sequence 663, Application US/10295027
Publication No. US2003023230A1
GENERAL INFORMATION:
APPLICANT: Afar, Daniel
APPLICANT: Aziz, Natasha
APPLICANT: Ginsberg, Wendy M.
APPLICANT: Glah, Kurt C.
APPLICANT: Glynn, Richard
APPLICANT: Hevezl, Peter A.
APPLICANT: Mack, David H.
APPLICANT: Murray, Richard
APPLICANT: Watson, Susan R.
APPLICANT: Eos Biotechnology, Inc.
TITLE OF INVENTION: Methods of Diagnosis of Cancer, Compositions and
TITLE OF INVENTION: Methods of Screening for Modulators of Cancer
FILE REFERENCE: 018501-012500US
CURRENT FILING DATE: US/10/295,027
CURRENT FILING DATE: 2002-11-13
PRIOR APPLICATION NUMBER: US 09/663,733
PRIOR FILING DATE: 2000-09-15
PRIOR APPLICATION NUMBER: US 60/350,666
PRIOR FILING DATE: 2001-11-13
PRIOR APPLICATION NUMBER: US 60/335,394
PRIOR FILING DATE: 2001-11-15
PRIOR APPLICATION NUMBER: US 60/332,464
PRIOR FILING DATE: 2001-11-21
PRIOR APPLICATION NUMBER: US 60/334,393
PRIOR FILING DATE: 2001-11-29
PRIOR APPLICATION NUMBER: US 60/340,376
PRIOR FILING DATE: 2001-12-14
PRIOR APPLICATION NUMBER: US 60/347,211
PRIOR FILING DATE: 2002-01-08
PRIOR APPLICATION NUMBER: US 60/347,349
PRIOR FILING DATE: 2002-01-10
PRIOR APPLICATION NUMBER: US 60/355,250
PRIOR FILING DATE: 2002-02-08
PRIOR APPLICATION NUMBER: US 60/356,714
PRIOR FILING DATE: 2002-02-13
Remaining Prior Application data removed - See File Wrapper or PALM.
NUMBER OF SEQ ID NOS: 1386
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 663
LENGTH: 1627
TYPE: PRT
ORGANISM: Homo sapiens
US-10-295-027-663

Query Match 45.5%, Score 3916.5, DB 15, Length 1627,
Best Local Similarity 45.8%, Pred. No. 8.8e-297,
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

Db 198 YLAATYDQFMKLVYNGAQAATSGEYGGISPLTQCKNVLMLG--SALHNHRYGIEH 255
Qy 193 LVFSTALPQSHFQSSGSEBEADTVLTASPEPVNTEVPFRDEKRYLREV--LQG 250
Db 256 FSLMKVARTQREILSDMETHGAHTALPQLLENNMDNVKHAMSPKQSSPKVERSNHG 315
Qy 251 FEPEELISPLQPLCGQTVCDNVELISQNGVYPLGEEKYIRYQVNNICDEGLNPFVS 310
Db 316 FLDD---TSLPEPLCGQTLCDNTEVIASYNQSSFPQPKVRYRVNVLVBDDHKNPVT 371
Qy 311 BEQIRLOHEALNBAFSRNYNSMQLSVHQVHNSTLRHRYLVNLCSPKSGNDHCEPCEHP 370
Db 372 REQVDFQHOLAARFKQYNISMELDVLEVSNSLRRLILANCDISKIDENCCBECHHT 431
Qy 371 LTYDGDGDCR-LQGRCSYWNRRDGLCHVECNMMLNDPDDGCDPPQVAVKTCFDPSP 429
Db 432 LTGHGDDGCRHLRHPAFVKQHNVCMDYERFNFQDGCEDPEITNVTQTCTFDPSP 491
Qy 430 KRAYMSYKELKALQLNTHFLNTYFASVVEDLAGAATWMDADAVTHLGIVLSPAYY 489
Db 492 HRAVLVNEELKNILKLDGSTHLNTPAKSSBEELAGVATWPMDEKALMHLGIVLNPFFY 551
Qy 490 GMPGHTDMIEGVHVLGLYVFPKGVSEBSCNDPCKETVPSMETGDLCACTAPPKSEL 549
Db 552 GMPGHTDMIEGHSLGLYVFPKGVSEBSCNDPCKETVPSMETGDLCACTAPPKSEL 611
Qy 550 CREPEPTSDTCGTPFPAPPTNYSYTDNCTNFPNQVARNHCYLDLVYQOWTESRK 609
Db 612 CGDGPNGDTCGFHSFNTFPNNFMSYADDCTDSTFPNQVARNHCYLDLVYQOWTESRK 671
Qy 610 PTPPIPPMVGQTNKSLITIMLPPISGVYVDRASSGLCGACTBEDGTFRQYVHTASSRV 669
Db 672 PAPALAPQVLTGHTDSTVLEMPPIIDGHPFERELGSCACHLILVQVASSSSPMP 731
Qy 670 CDSGQWTPREAVPVPVDPDCEPSLQAMSEVHLNHNMMVPP-TEGCSLELFOHP 728
Db 732 CSPSGHWSPREABHPVDEOPCKSSVKTSNSANAPHTVPACBPBGCTLEBFLPL 791
Qy 729 QADTLTLMVT--SPFMSSQVLPFTEILLENKESVHLGPLTDCDIPLTILK-HVHGKYS 785
Db 792 VPESLTIWTFVSTIDMSSGAVNDIKLLAVSGKISLQPGVAFCDVPLTILMVDGEVY 851
Qy 786 GVKYTFDERIEDAALLTSQPSPLCSGCPVRYQVLRDPPFASGLPVVVTSHRKFTD 845
Db 852 GIQYTLDEHLEIDAAMLTSTADPLCLQCKPLKTKVVRDPLQMDVASIL-HNKRKEVD 910
Qy 846 VEVTGQMYQVYLAELAGELGEASPLNTHNAGPYCGDGKVSRLGEECDGDLVSDG 905
Db 911 MDNLGSGVYQVWVTTISGTSEBSPSPVYTHGSGYCGDGI IQDQGEQCDMMKINIDG 970
Qy 906 CSKVCLEBEGFNCGEPSLCYMEGDCICEPFEKTSIVDCGYTPKGYLDQMAVRAVS 965
Db 971 CSLFCRQEVSNICDEBSRCYFHGDGDCVEFEKTSIKCGGVYTPQGFDDOMASNAVS 1030
Qy 966 HEDKKKCPVSLVTEP-HSLICTSYHDPLEPHRPLTGMFCVASENETQDTRSOPBSGL 1024
Db 1031 HQD-QQCPGWYIIQOPASQVCRTKVIDLSEGISQHMWYPCISYPSQ----- 1078
Qy 1025 KKEDEVWLKVCFNRRGABAFIFLITDGLVPGHQPTVLYLTDVRGSHSISGTGLS 1084
Db 1079 LAQTFMLRAVFSPPMAAAYVHLVTDGYTYGQOKETTSVQLDPTDQSHDGLHLVLS 1138
Qy 1085 COHNPILINVTNHNQVLFHHTSVTLNLFSSPBGVISAVALRTSRIGLSAPNSCISEDEG 1144
Db 1139 CRNNPLIIPVHDLDSQGFYHSAVRSFSSGLVAISGVALRSFNNPVPVLTSSC-QGGET 1197
Qy 1145 QNHQGSCTIRPCKQKQSCSLLDHADVNCSTI---GRLMKCAITQREGALQASS 1200
Db 1198 YSPABQSCVAFACKCTD-CELAVERNAS-LNCSSSDRYHG---AQCVYSCGTGYLQTR 1252
Qy 1201 GQYRPMQ--KEILTLTSSGHWMDQNSCLPVDGCVPPSLVNVNPFSCSEGTKFLKQCSI 1258

Dh 1253 DDELIKSGTSPVTVCTEGKMNKQVACEPYDCSIPDHQVYAASFSCSEGTTFGSCSF 1312
Qy 1259 SCVPRATQSGSPMLTCLBDMLSLPRVYCKLEBDAPRIILNANLLPHLCODNHVCTI 1318
Db 1313 QCRHPAQKGNNSLLTTCMEDGLMSFPEALCELMCLAPPVPAADLQTRARENHKGXSP 1372
Qy 1319 CKYCKCPGYVAESAEGKVRNKLTKIOCLEGGIWEQSGCIPVCEPPRPVEGMYECTNG 1378
Db 1373 CKYCKCPGYHVPSSR-KSKRAFAKTQCTODGSMQEGACVPTCDPPRPKHGLYQCTNG 1431
Qy 1379 FSLDSQCVLNC-----NOERKLPILCTKEGLMTOEFKLCENLQGECPRPPELNS-VEX 1432
Db 1432 FQFNSGCRKICEDSDASQGLSGSNVYHCKRDKGTWNGSFVCCOMOGOC-SVNEBELNSMLK 1490
Qy 1433 KCEBGYGI GAVCSPLCVIPSGDPVWL PENITADLTLEHMEBPVKOSIVCTGRBQMHDPV 1492
Db 1491 QCPDGYALGSECAATSCLDHNSSEIILPMNVTVRDI PHMLNPTREVRVCTIGLKYRHPA 1550
Qy 1493 LVHCIOGCEPFOADGMCDDTINNRAVCHYDGDCCSSTLSKKVI PFAADCDD-ECTCRD 1551
Db 1551 LHCYKCGEPPMGNDYCDAINNRAFCNVDDGCCCTSTYKTKKVPFPMSCDLQGDCACRD 1610
Qy 1552 PKAEN 1557
Db 1611 POAQBH 1616

RESULT 10
US-10-783-311-1
; Sequence 1, Application US/10783311
; Publication No. US20050009136m1
; GENERAL INFORMATION:
; APPLICANT: Nixon, Andrew
; TITLE OF INVENTION: PAP-A LIGANDS
; FILE REFERENCE: 10280-059001
; CURRENT APPLICATION NUMBER: US/10/783, 311
; CURRENT FILING DATE: 2004-02-19
; PRIOR APPLICATION NUMBER: US 60/448, 515
; PRIOR FILING DATE: 2003-02-19
; NUMBER OF SEQ ID NOS: 394
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1627
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-783-311-1

Query Match 45.5%; Score 3916.5; DB 17; Length 1627;
Best Local Similarity 45.8%; Pred. No. 8.8e-297;
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

Qy 16 REAETPNSQVLP--ILYSGRRERL-LRPEVLAIPREAFVYEAWYKPGGONNPAII 72
Db 80 REAGATEPEPPPSRALYFSGRGEQLRVLRADL--ELPRDAFTLQVWMLRAEGGORSPIVI 137
Qy 73 AGVDNCSHTYSDGKMGALGIRSGDKGRDARFPESLCTDRYKATILISHSRQOPTWT 132
Db 138 TGLYDKCSYISRRDKGVVGHHTISDQDKDPRYFSLKTDRAQVYTTINARSYLPQGV 197
Qy 133 HVAATYDRAHVALYDGTQVASSLDQSGPLNSPFMACSRLLGLDSESDGHYFRGLGT 192
Db 198 YLAATYDQPKLYVNGAQTSGEYGVGIFSLQKRYLMLGG--SALNHNTRYIEN 255
Qy 193 LVFWSTALPQGHFQHSQSSGSEEBATDLVLTASFEPVNTWVPREDKYRLLEV--LQG 250
Db 256 FSLWKVATQREILSDMETGHATLPLQLIQENWMDNVKHAMSPKDDSSKVEFSNANG 315
Qy 251 PEPEPEILSPQPLCGQTCVNDNELLISQNGVMPRLREKVIYRQVNNICDDEGLNPIYS 310
Db 316 FLDD---TSLPEPLCGQTLCDNTEVLAASYNQLSSFQPKVVRVNVLYEDHKNPVT 371
Qy 311 BEQIRLQHEALNEAFSRNYSIMQLSVHQVNSTLHRVVLVNCBPSKIGNDCHDCEBEP 370

Dh 372 REGVDFOHQDLAERFAKQYNISWEIDVLEVSNSILRRLLIANDDISKIGENCEPCENHT 431
Qy 371 LTGYDGGDCR-LQGRCSNMRRDGLCHVECNMNLNDDDDCCDPQVADYRKTCFDDSP 429
Db 432 LTGHIDGDCRHLHRAVKKQHNGBVCDMDCNFERFNDDGBCDPELTNTVQTCFDDSP 491
Qy 430 KRAVMSYKELKEALQUNSTHFLNIYFASVYREDLAGAATPMDKADATHLGIVLSPAY 489
Db 492 HRATLDVNEKLNILKUDGSHLINI PFAKSSSEBELAGVATPMDKALMLHGGIVLNSFY 551
Qy 490 GMRGHTDMHEGVHVLGLYHFKGVSERSCNDPCKEYVPSMETGLCADTAPPESEL 549
Db 552 GMRGHTMTHEIGHSLGLYHFRGISLEIOSCPDPEETPSEFETGLCDNTVPAPRKS 611
Qy 550 CRREPESTDGCFTRFEGAPFTYMSYTDNCTDNFTPNQVARNHGYLDLYOOQWESRK 609
Db 612 CGDPGENDTCGRHSFNTYNNFMSYADDCTDSFTPNQVARNHGYLDLYOQWESRK 671
Qy 610 PTPPIPMWYIGOTNKSLLTHMLPRLSGVYDRAAGSLGACTEDGTFRQYVHTASSRV 669
Db 672 PAPALAPQVLGHTTDSVLEWPPRIDGHFERELGACHLCLEGRILVQYASNASBMP 731
Qy 670 CDSGWTPEEAVGPPVDQPCPSLOAMSPEVHLIYHANNVPCP-TEGCSLELFPQHV 728
Db 732 CSPSGHWSPREAEGHPVDEQPCKSSVWTSPNSAVNPHVTPACPEPQGCYLELEFLYPL 791
Qy 729 QADTLTMTV--SFMSSQVLPDTEILLEKNSYHGLDTCDDIPLTKL-HVDKVS 785
Db 792 VPSLTIWTVFVSTDWSSGAVNDIKLAVSGKNISGPPNVNCDVPLTRLMDVGEVY 851
Qy 786 GVKVYTFDERLEIDAALLTSQPHSPLCSGCRPVRYQVLRDPPASGLPVVVTSHRKFPTD 845
Db 852 GIGYITLDEHLEIDAALLTSTADTPLCQKPLKYKVRPPIQMDVASTL-HNKRFPVD 910
Qy 846 VEYTPGMYQYVLAERAGSELGEASPLNHHGAPYCGDGKVSBRIGECDDGDVSGDG 905
Db 911 MDNLGSGVYQWVLTISGTESESPSPAVTYIHGQYCGDGIQKQDQEQCDMMKXINGDG 970
Qy 906 CSKYCELEBGFNCGEBSLCYMYEGOGICPEPRKTSIVOCGYITPBGYLDOMATRAYSS 965
Db 971 CSLEGRQEVSNFCLDESRICYFHDGDVCEFPQKTSIKOCGYVTPGSPFLDOMASNASVS 1030
Qy 966 HEDKCKCPVSLVTGEP--HSLICTSYHPLDPMHRPLTGMPCVASENETQDRSBOPEGST 1024
Db 1031 HQD-QQCPGVIIIGPAPASQVCKTKVIDLSEGISQAHMYCTISYPSQ----- 1078
Qy 1025 KKEDEVMLKVCENRPGEARAIFLITTDGLVPGEHQOPTVLYLTDVRSNHSIGTYGLS 1084
Db 1079 LAQTFWLRAVFSQPMVAALVIVHLYTDGYTGQKQETISVOLLDTKDQSHDGLHVLVS 1138
Qy 1085 QCHNPLIINTHQNVLFEHHTTSVLTNFSRPVIGISVALRTSRIGLASPMNCISDEG 1144
Db 1139 CRNNPLIIPVHDLISQFVNSQAVRSFSSPLVAISGVALRSFDPNEDVTLSSC-QRGET 1197
Qy 1145 QNHGOGSICRPGCKODSCPSLLDHDADVNTCSI-----SPGLMKCAITQORGFALQASS 1200
Db 1198 YSPRQSCYAFACEKD-CBELAVENAS-LNCGSSDRYHG--AQCVSQRGTGVLLDIR 1252
Qy 1201 QGYIRPMQ--KEILLTSSGHWMDONVSCLPVDCGVPDPSLVNTANFSCSBGTKFLKCSI 1258
Db 1253 DDELIKSGTSPVTVCTEGKMNKQVACEPYDCSIPDHQVYAASFSCBGTTFGSCSF 1312
Qy 1259 SCVPRATQSGSPMLTCLBDMLSLPRVYCKLEBDAPRIILNANLLPHLCODNHVGTI 1318
Db 1313 QCRHPAQKGNNSLLTTCMEDGLMSFPEALCELMCLAPPVPAADLQTRARENHKGXSP 1372
Qy 1319 CKYCKCPGYVAESAEGKVRNKLTKIOCLEGGIWEQSGCIPVCEPPRPVEGMYECTNG 1378
Db 1373 CKYCKCPGYHVPSSR-KSKRAFAKTQCTODGSMQEGACVPTCDPPRPKHGLYQCTNG 1431
Qy 1379 FSLDSQCVLNC-----NOERKLPILCTKEGLMTOEFKLCENLQGECPRPPELNS-VEX 1432


```
RESULT 12
US-10-991-321-32
; Sequence 32, Application US/10991321
; Publication No. US20050112675A1
; GENERAL INFORMATION:
; APPLICANT: Rosinski, James Peter
; APPLICANT: Koehen, Jarema Andrew
; TITLE OR INVENTION: Specific Markers for Metabolic Syndrome
; FILE REFERENCE: 21742 US1
; CURRENT APPLICATION NUMBER: US/10/991,321
; CURRENT FILING DATE: 2004-11-17
; NUMBER OF SEQ ID NOS: 36
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 32
; LENGTH: 1627
; TYPE: PRN
; ORGANISM: Homo sapiens
US-10-991-321-32

Query Match      45.5%; Score 3916.5; DB 17; Length 1627;
Beet Local Similarity 45.8%; Pred. No. 8.8e-297;
Matches 718; Conservative 296; Mismatches 499; Indels 53; Gaps 25;

Qy 16 REAETPNSQVGLP--IIYFSGRBRRL-LLRPEVLAEIPREAFTEAWKPEGGONPAII 72
Db 80 REAGATEBEPSPRALYFSGRGQQLVRLADL--ELPRDAFTLQWMLRAGGQSRSAVI 137
Qy 73 AGVPDNCSTHVSDKGMALGIRSGDKGRARFFPSLCTDRVKATLIIISHRYQPGTWT 132
Db 138 TGLYDKSCSYISRDRGMVVGIIHTISDQDKDPRYFSLKTDRAQVTTINARSYLPQWV 197
Qy 133 HVAETGYRMAALVVDGQVAVSSLDGSLNSPMASSRLLDGDSSEDDHYRGLIGT 192
Db 198 YLAATYGGQFKLYNAGVATSGEQVGFSPLTQCKVLMG3--SALNHNRYIEH 255
Qy 193 LVFSTALPQSHFQSSGSEBEATDVLTLASFEPNTEWVFPREDKYRLLEV--LOG 250
Db 256 FSLMKVARTQREILSDMETHAHTALPQLLOENWMDVAKHMSFMKQSSSKVFSNAG 315
Qy 251 FEPPEILSPLOPLCGQTCVNDVELISQYNGWPLRGEKYRYQVANI CDDEGLNPIVS 310
Db 316 FLDD---TSLPEPLCGQTLCDNTEVILASYNQLSSFPQPKVRYRVNVL YEDHKNPVT 371
Qy 311 EEOURLHEALNEAFSRYNISMOISVQVHNSITLRHVVLVNCSPKXIGNHCDBECP 370
Db 372 REQVDFQHOLAFAFKQYNISWELDVLEVSNSLRRLILANCDISKIGDNCDPBCNHT 431
Qy 371 LTYDGGDCR-LOGRCYSWNRDGLCHVECNMNLNDEPDGDCDPOVADYRKTGCFDPS 429
Db 432 LTGHGGDCRHLRPAFKQKHNGVCMDCNVERFNPFGGSCDPELITNVQTGCFDPS 491
Qy 430 KRAYMSYKELKALQLNSTHFLNLYPASVREDLAGAATWPDWDXDVAITHLGGIYLSPAY 489
Db 492 HRAVLDAVELKNIILKDGSTHLNIFPAKSEBELLAGVATWPDWDEALMHLGGIYLSNPFY 551
Qy 490 GMPGHTDMHEVGHVGLYHVFKGVSRESNDPCKETVPSMETGSLCADTAPRSEL 549
Db 552 GMPGHTDMHEIGHISGLYHVFGRGISLQSCDPCHETESPFTGDLCDNTNAPRHS 611
Qy 550 CRBEPTSDTCGTFRPGAPFTNTMSYTDNCTNFTPNQVARNAGCYLDLVYQOMTESRK 609
Db 612 CGDGPNGDITCGHFSFNTPNNMMSYADDDCTDSFTPNQVARNAGCYLDLVYQOMQSRK 671
Qy 610 PTPPIPPMVIQGNKSLITIMWLPPISGVVYDRASSGLCGACTEDGTFRQYVHTASSRV 669
Db 672 PAPALAPQVIGHTTDSVTLTWPFPIDGHFPEREIRGSACHLCEGRILIVQYASNASBMP 731
Qy 670 CDSGYMTPREAVGPDPVDCPSLSQAMSEVHLIYHNMNVVPPR--TEGSGLELFPQHV 728
Db 732 CSPSGHMSPREABGHDPVQPCSSVKTWSPNSVNPHTVPACBPQGCYLELEFYPL 791
Qy 729 QADTLTLMVT--SFFMESSQVLPDTEILLNKESVHLGPLDTPCDIPTIKL-HVDDKVS 785
```

```
Db 792 VPESLITWTFVSTDMDSGA VNDIKLANVSGKNISLGPQNVFCVPLTIRLMDVGEVY 851
Qy 786 GVRVYTFDERIETIDALLTSQPHSLCSGCRPVRYQVLRDPPRAGSLPVVYTHSHKFTD 845
Db 852 GIOIYTLDEHLEIDAMLTSTADTPLCTCKPKRYKVRDPPQOMVASTL-HLNRKFVD 910
Qy 846 VEYTPGOMYQVYLAEBAGELGASPLNHHGAPYCGDGKVEERLGECCDDGLVSGDG 905
Db 911 MDNLGSLVQYWIITISGTESESPAVYIYHGRGICGDI IQKDQEGCDDMNKINGDG 970
Qy 906 CSKYCELEBGFNCVGBESLICYMEGDI CFPFERKTSIVDGIYTPKGYLDQATRAYSS 965
Db 971 CSLFCRQEVSFNCIDERSRCYFHDGQVCSEFRKTSIKDCGVYTPQGFIDQASNASVS 1030
Qy 966 HEDKCKPVSLVNGEP-HSLICTSYHDLPHNRPLTGWPFQVASENETQDRBEQBGSL 1024
Db 1031 HQD-QQCPGVIIIGOPASQVCRKVI DLSEGISQAHWPCTTISYPSO----- 1078
Qy 1025 KKEDEWMLKVCFNRPGBARAFIFLTTDGLVPGEHQOPTVTLTYLTVRGSNHSIGTYGLS 1084
Db 1079 LAQTTMLRAVFEQPMVAANAVIYHLVTDGYIDQKQETISVGLDITKQSHDLGLAVLS 1138
Qy 1085 CQHNPILINVTYHQNVLFHHITSVLLNFSSPRVGISAVALRTSSRIGLSAPNSCISEDG 1144
Db 1139 CRNPNLIIIPVHDLQPFYHSAVRVSFSSPLVAISGVALRSPDNFPVTLSSC-ORGET 1197
Qy 1145 QNHQGSCTHRPCGKODSCPSLLDHDADVNCISI---GRLMKCAITQGRPALQASS 1200
Db 1198 YSPAEOCSVHFAEKTQD-CELAVENAS-LNCSSSDRYHG--AQCTVSCRTGYVQIR 1252
Qy 1201 GQYIRPMQ--KEILTLCSGHWONVSCLPVDGVPDPSPLVNANYANFSCSEGTFLKRCST 1258
Db 1253 DDELISKSQIPSTVYICTBEKNMKQVACERPYDCSIRDHQVYASFSCEPRTGFGQCSF 1312
Qy 1259 SCVPAKQGLSPMLTCLBEDGLMSLPVYCKLECDAPPIILNANLLPHCLQDNHDVGTI 1318
Db 1313 QCRHPAQOLKNNLSILTCMEDGLMSPEALCELMCLAPPVPNADLQIARCREKNHKVGSF 1372
Qy 1319 CKTECKRGYVVASAEGKANKLKTQCLBGGIWEQSSCI PVYCEPPRPVPEBMYECTNG 1378
Db 1373 CKYCKRGYHVPSSR-KSKRAFKYQCTQDGSWQBARCAPVYCDPPRPFGLYQCTNG 1431
Qy 1379 FSLDSQCVLNC-----NOEREKLPILCTKEGLTQEFKLCENIQGBCPPPSBLANS-VEX 1432
Db 1432 FQNSEERICCEBDSASQGLGNSVHICRDKGTNGSFHVCQEMQGC-SVFNLSNINLKL 1490
Qy 1433 KCBQYIGIGAVCSPLCVIPSPDFVMLPENITADTLBHMEPVKQSI VCTGRQMHDPV 1492
Db 1491 QCPDGYALISGECATSCIDHNSESIILPMNVTVADIDPHMLNPTREVERVCTAGLKWYBHPA 1550
Qy 1493 LVNHCISCEPFQADMCNCTINNA YCHYDGGDCSSSTLSKXYIPFADCDLDL-ECGCRD 1551
Db 1551 LHHVCGCEPFMDNVCDAINNPACFNVDGDCCTSTVTKTKVTPPMSCDLGGDCACRD 1610
Qy 1552 PKAEN 1557
Db 1611 PQAQEH 1616

RESULT 13
US-10-887-229A-8
; Sequence 8, Application US/10887229A
; Publication No. US20050148509A1
; GENERAL INFORMATION:
; APPLICANT: DAKE, BRIAN
; APPLICANT: BOOTH, BARBARA
; APPLICANT: BOES, MARY
; APPLICANT: BAR, ROBERT S.
; TITLE OR INVENTION: BINDING PROTEINS AS CHEMOTHERAPY
; FILE REFERENCE: IOMA:049US
; CURRENT APPLICATION NUMBER: US/10/887,229A
; CURRENT FILING DATE: 2004-07-08
```

```

PRIOR APPLICATION NUMBER: 60/538,000
PRIOR FILING DATE: 2004-01-21
PRIOR APPLICATION NUMBER: 60/485,846
PRIOR FILING DATE: 2003-07-09
NUMBER OF SEQ ID NOS: 16
SOFTWARE: Patent Ver. 2.1
SEQ ID NO 8
LENGTH: 1627
TYPE: PRT
ORGANISM: Homo sapiens
US-10-887-229A-8

Query Match      45.5%; Score 3916.5; DB 18; Length 1627;
Best Local Similarity 45.8%; Pred. No. 8.8e-297; Index 53; Gaps 25;
Matches 718; Conservative 296; Mismatches 499;

Qy 16 REAETFSQVGLP--ILYSGRRRL-LRREVLAIEREAFTVEAWKPEGGQNNPAII 72
Db REAGATEEPSPSPRALYFSGRGELRVLRADL--ELPRDAFTLQVWLRAGGGRSPAVI 137
Qy 73 AGVDNCSHTVSDKGMALGIRSGDKGRDARFFPSLCTDRYKATILISHRYQPGTWT 132
Db TGLVDKCSYISRDGWWVGIHTISQDNKDRYFPSLKTDRARQVTTINARSYLPGQVW 197
Qy 133 HVAATYDGRHVALYVDGTQVASSLDGSGPLNSPFASCRSLIGDSSEDEGHYRGHIGT 192
Db YLAATYDQGFEMKLYNQAQVATSGVGIGTSPLOKCKVLMGQ--SALNHNRYGIEH 255
Qy 193 LVFMSIALPQSHFQHSQSSGSEBATDVLVTASFEVNTMEVPRDEKRYRLVY--LQG 250
Db FSLKVAARTQREILISDMETHGAHTALPQLLOEMMDNVKHAMSPKQSSPFVEFSNMG 315
Qy 251 FEPEPELISPLQPLCGQTCVDNVELISQYNGWYPLRGEKVIYRQVNI CDDEGLNPIVS 310
Db FLDP-----TSLEPLCGQTLCDNTEVLASYQLSSFPQKVVRYRVVLYEDDHKNPTVT 371
Qy 311 EEOIRLOHEALNEAFSRYNISMO:SVQVHNSTLRHRYLVNCEPSKIGNHCDCPECHP 370
Db REQVDFQHHQALAEFAKQYNISWELDVLEVSNSLRRLILANCSIKGIDNCPBECNHT 431
Qy 371 LTGYDGDRCR-LQGRCYSMNRDGLCHVENNMNLNDFDGDCCDPOVADVKTCTCFDPSP 429
Db LTGHGDGDCRHLRPAFYKQKANGVCMDCYERFNPBGSCCPBEINVTQCTFDESP 491
Qy 430 KRAYMSYKELKALQLNSTHFLNLYPASVREDLAGAATWPDMDXAVTHLGIYSPAY 489
Db HRAVLAVNELKNIKLKDGSTHLNIFFAKSSSEELAGVATWPMDEKALMHLGI VLNBSFY 551
Qy 490 GMPGHTMTHEVGHVGLYHVPKGVSRSCNCPCKETVPSMETGDLCDATAPTPKSEL 549
Db GMPGHTMTHEIHSGLYHVPFGISIQSCDPCMETEPPSFTGDLCDNTPAPKHS 611
Qy 550 CREBEPTSDTCGTFRPGAPFTNMYSYTDNCTNFTFNQVARNHCYLDLVYQOOTESRK 609
Db CGDGPNDTCGHSFNTPYNNMYSYADDCITCSFTFNQVARNHCYLDLVYQOOTESRK 671
Qy 610 PTPPIPPMVIIGQTKSLTIHMLPPISGVYVDRASGSLCGACTEDGTFRQYVHTASSRV 669
Db PAPVALAPQVGHGHTTDSVTLEMPPIIDGHFERELSGSCHLCTEGRILIVQYASNASBMP 731
Qy 672 CDSSGYMTPBEAVPRVUDOCSEPSLOAMPSEVHLHNMNVPRP--TEGCELELTFQHPV 728
Db CSBPGHMSPREABGHVPDPCSSVVRWSPNSAVNPHTPAPCAPPEPGCYLLEFLYPL 791
Qy 729 QADTLTAMVT--SEFMSSQVLFPTTEILLENKESVHLGPTLFCDIPITIKL-HYDGVIS 785
Db VPBSLTIWTFVSTDMWSSGAVIDIKLLAVSGKNI SLGQVNVFCDFVLTITLWVGERVY 851
Qy 786 GVAVYTFDERIEDAALITSGPHSLCSGCRPVRYQVLRDPPASGLPVVVTSHRRKTD 845
Db GIQYTLDEHLEIDAMLTSTADTPLCIQCKPLKVKVVRDPLQMDVASIL-HLNRRKVD 910
Qy 846 VEVTRGMVYQVLAELAGELGEASPLNHTHGAPYCGDGKVSRLGECCDDGLVSGDG 905

```

```

Db 911 MDNLGSGYQVWYTTISTESESPPATYIHNGVCGDGIQIQDQSGCDDMANKINDG 970
Qy 906 CSKYCELEBEGFNCVGBEPLCYMBGDI CEPPERTKTSIVDCGIYTPKGYLDOMATRAYS 965
Db CSLFCRQEVSNFCIDEPBRCYFHDDGVCEFEQKTSIKDCGVYTPQGFLOQMNASVVS 1030
Qy 966 HEDKKKCPVSLVTEBP-HSLICTSYHPLPMHRPLTGMFPCVAVSENEQDDRSEDESSL 1024
Db HQD-QQCGGVWIIQOPASQVCRKTVIDLSEGISQAHAWYPCITISVYSQ----- 1078
Qy 1025 KKEDEWMLKVCENRPGEARAIFILTTDGLVPGEHQPTVLYLTDVGNSHSLGTGSL 1084
Db LAQTFMLKRAFSGPMAAAVIVLVDGTYYGQKQETISVQLDPTDQSHDLGHLVLS 1138
Qy 1085 QONNPLIINTVTHQNVLFPHHTSVLNFSSPRVIGISAVALTSSRIGLSAPSNCISDEG 1144
Db CRNPLIIPVYHDLQPFYHQAVRVSFSSPLVVISGVALRSPNFPDVTLSSC-QRGET 1197
Qy 1145 QNHQGSQCIHRPCQKQOSCESSLDDHADVNVCTSI---GRLMKCAITTCQGFALQSS 1200
Db YSPAEGSCVHPACEKTD-CPELAVENAS-LNCSSSDRYH--AQCTVSCRTGYVLQIR 1252
Qy 1201 GQYIRPMQ--KEILLTSSGHDQNVSCLPYDCGVPPSLVNVANFSGSEGTFLKRCST 1258
Db DDELKSGQTSVYVTTCTEGKMKQVACEPVDCSI PDHQAUYAASFSCPEGTITGSGQSF 1312
Qy 1259 SCVBPARKLGSLPWLTCLEDLGWSLPEVYCKLECDAPRIILNANULLPHCLQDNHDVGTI 1318
Db QCRHPADLKGNNSLLTTCMEGLWSFPEALCSLMCLAPRPVADLQTRAGENHKKVGSF 1372
Qy 1319 CKYCKKGYIYABEAGKVRNKLKIQCLBSGIEQGSCLIPVCEPPPVVEGMYECTNG 1378
Db CKYCKKGYHYPGSSR-KSKKRAFKTCTOPGQWQBGCVVTCDDPPPKHGLYQCTNG 1431
Qy 1379 FSLDSQCVLNC-----NOERKPLILCTKESLMTQEFLLCENLQGECPPESSLNS-VEX 1432
Db FQNSBCKIKCEDSDASQGLASNVIHCKDQSTWMSFHVCEMGOQC-SVENELSNLKL 1490
Qy 1433 KCEQYGVIGAVCSPLCVI PPSDPVMLPENITADTLKHMMEVVKQSIYVCTGRROWHPDV 1492
Db QCRPGVIAIGSECAISCLDNHSEIILPMNVYVRDI PHMLNTRVBRVYCTGAKMYRPA 1550
Qy 1493 LVHCIOGCEPPOADGKCDTINRAYCHYDGDCCSSTLSKKVLPAAACDL-D-ECTGRD 1551
Db LHHCVKCEPFGMDNYCDAINNRAFCNVYDGDCTSTVTKKVTYPPFWSCDLQGDCACRD 1610
Qy 1552 PKAREN 1557
Db 1611 PQAOEH 1616

RESULT 14
US-10-783-311-2
Sequence 2, Application US/10783311
Publication No. US2005009136A1
GENERAL INFORMATION:
APPLICANT: Hoxan, Andrew
APPLICANT: Hoxan, Shannon
TITLE OF INVENTION: PAPP-A LIGANDS
FILE REFERENCE: 10280-059001
CURRENT APPLICATION NUMBER: US/10/783,311
PRIOR FILING DATE: 2004-02-19
PRIOR APPLICATION NUMBER: US 60/448,515
NUMBER OF SEQ ID NOS: 394
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 2
LENGTH: 1547
TYPE: PRT
ORGANISM: Homo sapiens
US-10-783-311-2

```

Query Match 45.5%; Score 3914.5; DB 17; Length 1547;
 Best Local Similarity 46.1%; Pred. No. 1.2e-296;
 Matches 714; Conservative 295; Mismatches 420; Indels 51; Gaps 24;

30 LYESGRRRL-LARPEVLAETIPREAFTEAWVKRGGONNPALIAGVFDCNSHTVSDKW 88
 16 LYESGRRRL-LARPEVLAETIPREAFTEAWVKRGGONNPALIAGVFDCNSHTVSDKW 73
 89 ALGIRSKDKKRRAPRPFSLCTDRVKKATLLISHSRVQPTWTHVATYDGRMALVYD 148
 74 VGIHTISDDNDKPRYFSLKTRARQVITINARSLTPGOWYLLATYDGMKLYVN 133
 149 GTQVASSLDSGSPINSPFMASSRSLILGSDSSBDGHYFRGLITLVFWSTALPQSHFQHS 208
 134 GAQVATGEOVGIGFSPILQCKYLMIG--SALNHNRYGIEHPSLWKVARTRELLSD 191
 209 SQHSSGEEATDVLITASFEFVNTWVPFRDEKYPRLV--LQGFPEPELISPLQPLC 266
 192 METGATHTALPQLLQEWMDVVKHAMSFMKDGSSPKVEFSNAHGFLD---TSLRPLC 247
 267 GQVYCDNVELISQYNGWPLRGEKVIRYQVNNICDDGLNPVSEGOIRLOHEALNFAFS 326
 248 GQTLCDNTEVLASYNQSSFRQPKVVRVNNLYEDHKNTPTREQVDFQHOLAFAFK 307
 327 RYNISQOLSVHQNSTLRHRYVLVNCERPKIGNDHCDPECEHPLTGYDGGCR-LQGRC 385
 308 QYNISWELDVLEVNSSIRRLILANCDISKIGBENDCEONHTLTGHDGDCGHLNHPA 367
 386 YSMNRDGLCHECNMNLNDFDGDCCDPOVADYKTCFDPDSFKRAVMSYKEIKALQL 445
 368 FVKQHNQVCMDCNRYERFNDGECDDPEITNTVQTCFDPDSFHRAYLDVNEIKNLKL 427
 446 NSTHFLIYFASVREDLAAGATWPKDAATHIGVILSPAYYGMGHDTMHEYGHV 505
 428 DGSHTLNIFFAKSSSEELAGVATWPKDEKALMHLGGVILNPSFYGMPEHHTMHEIGHS 487
 506 LGLYHFKGVASERSSCNDPCKEATVPSMETGDLCAATAPTPSEELCREBEPTSDTCGFTRF 565
 488 LGLYHFKGVASERSSCNDPCKEATVPSMETGDLCAATAPTPSEELCREBEPTSDTCGFTRF 547
 566 PGAFPTVMSYTDNCTDNFTPNQVARNHCYLDLYQOMTESRKPPTPIRPMYIGQTNK 625
 548 FNTYNNFMSYADDDCTDSFTPNQVARNHCYLDLYQOMTESRKPPTPIRPMYIGQTNK 607
 626 SLTIHMLPTISGVVYDASGSLGACCTEDGFROYVHTASRRVCDSSGYMTPREAVQPR 685
 608 SVTLEWFPPLDGHFFERELSGACHLCLEGRILVOYASNASSPMFCSGHSMPREABGHP 667
 686 DVDQPCPSLQAMSPEVHLVHMNTVPCP--TEGCSLELLFQHPVQADTLTLMT--SFFM 742
 668 DVEQPCSSVATWPNASVNPHTVPRACRPPQGCYLELEFLYPLVPSLETLMTVFTSDW 727
 743 ESSQVLEPTEILLNKESVHLGRLDPTGDIPLTKL-HVDSKVSQVYVYTDDELEIDAA 801
 728 DSSGAVNDIKLVAASGKINISLGPONVFCVPLTRILMDVGEYVGIQIYTLDEHLEIDAA 787
 802 LITQSPHSLCSCGGRPVRYOVLDRPFASSGLPVVYTHSRKFTVEVTPGOMYOYULAE 861
 788 MLTSTADPLCLQCKPKTKVARDPLOMDVASIL-HLNKRFVDMDLASVYQITWYITI 846
 862 AGSELGASPEPLNIHGAPYCGDGKVSERLGEBCDDGDLVSGDGSKYCELEBGFNCVE 921
 847 SGTESERSPAVYTIHKGYGCGDGIQKMDGECDDMKINGDGSJLFCRQEVSPNCIDE 906
 922 PSLCYMTEGDI CEFPERKTSIVDCGYTPKGYLDQMATRAYSSHEDKKCPVSLVTGER 981
 907 PSRCYFHDGDCVCEFEQKTSIKDCGYVTPQGFILQWASNASVSHOD--QCCPGWVITIGOP 965
 982 -HSLICHSYHNDLNNHRLTGMPCVVASSENETODRSQPRGSLKDEYVAKCENP 1040
 966 AASGVCKRKYIDLSBGISQHAMYPCTISYPSQ-----LAQTFMLRAYFSQPM 1014
 1041 EARAIFLTLDGLVGRHQOFTVTLVYLDVGRGSHSLGTVGLSCQHNPLLIINVTYHQN 1100

1015 VAAAVIHLVTDGTYGQKQETISVOLLDTKQSHDLGHLVLSCRNNPLIIPVHDLISQ 1074
 1101 LPHHTTSVLLNPSPPVIGSAVALRTSSRTGLAPNSNCISEDGONNQGSCYHPCGKQ 1160
 1075 PFHSQVNRVRSFSSPLVAISGVLRSPDNDRPYTLSSC-ORGETYSABESCVHFACEKT 1133
 1161 DSCPSLLDHDADVNCSTSI----GPIGMKCAITCORFALQASSGOYIRPMQ--KEILLT 1214
 1134 D-CPELAVENAS-LNCSSSDRYHG---AQCTVSCRTGYVLQIRRDDELISQGTSPVTVT 1188
 1215 CSSGMDQNVSCIPVDCGVDPSELVNYANPSSCEBGTFLKRCSTSCYPRAKLOGLSWLT 1274
 1189 CTEGKNMKQVACBPVCSISDHHQVVAASPCBEGTIFGQCSFQCHHPQLKNNSLT 1248
 1275 CLFDGLMSLPEVYCKLECDAPRIILNANILLPHCLQDNHDPVGTICKCEKRGYVVAESA 1334
 1249 CMEDGLMSFPEALCEMLCLAPRPVPAADLTQACRKHKAVGSCFKYKCFGHVPPSSR 1308
 1335 GKYANKLLKIQCLEGGIWEQSGCIPVCEPPPVFEGMYECTNGFSLDSQCVLNC----- 1389
 1309 -KSKRAFKTQCTQDGSWQEGACVPVTCDBPPKFFHGLYQCTNGFQNSCRICKEDSDA 1367
 1390 NQERKLPILCTYBGLMTQEFKLCENIQCECPPPEPLNS-VEYKCEQYIGIAGVCSPLC 1448
 1368 SQGLSGNVICRDXGTWNGSFHVCOEWOQC-SVPELNLNLKIQCPDGYALISGECATSC 1426
 1449 VIPSPDPVMLPENITADTLTHMMPEVYVOSIVCTGRQOMHPDPLVHICQSCPEQADGW 1508
 1427 LDHNSSTIIPMNVYADIPHMLNPTFRVERVCTAGLKMTPHPLIHCVAGCEPFMDNY 1486
 1509 CDTINNRAYCHYDGDCCSSTLSSKVIYPPAADCLLD-ECTCRDPKAEN 1557
 1487 CDALINNAFCNYDGGDCSTSVTKTKYTPFPMSCDLQGDCACRDPAQEH 1536

RESULT 15
 US-10-741-600-1403
 ; Sequence 1403, Application US/10741600
 ; Publication No. US2005026169A1
 ; GENERAL INFORMATION:
 ; APPLICANT: CARGILL, Michele et al.
 ; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
 ; FILE REFERENCE: CLO01499
 ; CURRENT APPLICATION NUMBER: US/10/741,600
 ; CURRENT FILING DATE: 2003-12-22
 ; NUMBER OF SEQ ID NOS: 73997
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 1403
 ; LENGTH: 1420
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-741-600-1403

Query Match 41.8%; Score 3602; DB 17; Length 1420;
 Best Local Similarity 45.9%; Pred. No. 3.1e-272;
 Matches 659; Conservative 268; Mismatches 461; Indels 48; Gaps 22;

143 MALVYDGTQVASSLDSGSPINSPFMASSRSLILGSDSSBDGHYFRGLITLVFWSTALPQ 202
 1 MKLYNQAQVATSGEOVGIGFSPILQCKYLMIG--SALNHNRYGIEHPSLWKVARTQ 58
 203 SHFQSSQHSGEEATDVLITASFEFVNTWVPFRDEKYPRLV--LQGFPEPELISPLQ 260
 59 REILSDMETGATHTALPQLLQEWMDVVKHAMSFMKDGSSPKVEFSNAHGFLD---TS 114
 261 LQPLCGQVYCDNVELISQYNGWPLRGEKVIRYQVNNICDDGLNPVSEGOIRLOHEA 320
 115 LEPPLCGQTLCDNTEVLASYNQSSFRQPKVVRVNNLYEDHKNTPTREQVDFQHQ 174
 321 LNEAFSRINISQOLSVHQNSTLRHRYVLVNCERPKIGNDHCDPECEHPLTGYDGGCR 380

Dh	175	LAEAFKQNIISMEIDVLEVSNSLRRRLILANCOISKIDENCDCECHITLTHGDGBCR	234
Qy	381	-LQGRCYSMNRBDGLCHVECNMMLNDPDDGDCDQOVADVRKTCFDPDSPRAYMSYEL	439
Dh	235	HLRHPAFYKXOHNGCDMDCNVERFNFPGGCECDEBEITNVJOTCFDPDSPRAYUYDNVEL	294
Qy	440	KEALOLNTHFLNITYFASVREDLAGAATWMPMDKAVNHLGIVLSPAYCMMPGHTPMI	499
Dh	295	KNILLDOSTHNLNIFPAKSSBEELAGVATWPMDDKALMLHGLIVLNPSPFGMPGHTPMI	354
Qy	500	HEVGVLGLYHVPFKVSERESNDPCKETVSMETGDCADTAPRPKSELCREPERTSDT	559
Dh	355	HEIGHSGLYHVPFGISEIIOGSCDPCMETEBSFETGDCLDNTNPRPKKSGCDPERGNDT	414
Qy	560	CGFTRPFGAPRTNYSYTDNCTDNFTBNQVARMHCYLDLYVQWMTESRKPETPIRPMV	619
Dh	415	CGFHSFFTNPRYNNFMSYADDCTDFTBNQVARMHCYLDLYVQWMPERKXAPVALAQV	474
Qy	620	IGQNKSLITIMLPRISGVYITDRASGSLCGACTEGTGRQYVHTNHSRRVCDSSCYTPE	679
Dh	475	LGHITDSTYTLTWMFPRIIDGHFFERELEGSACHLCLBERILVOYASNASSPMPSPGSHMSR	534
Qy	680	EAVGPBDJOCSEBPLASPEYHLYHNMNTPCP-TEGCSLELFGHVPQADTLITMTV	738
Dh	535	EABGHDPDEQCKKSSVKTWSPNSANPRTPVPACBEPQCYLBEFLPLVPESLITMT	594
Qy	739	--SEFMSSQVLPDEILLENKESVHLAPLDFCDIPLTIKL-NDGKVSQVKVYTPFER	795
Dh	595	FVSTDMSSGAVNDIKLAVGKNISLGRQVNFCDVPLITILMVDGEVYGIQIYTTDEN	654
Qy	796	IEIDALITSGPHSPLCSGCRPVRYQVLRDPPRPSAGLFVVVTHSHRKTDEVTTPGQMY	855
Dh	655	LEIDAMLTSTADPRLCQCKRPLKXVVRDPLQMDVASIL-HLNRKKVMDMLNGSYQ	713
Qy	856	YQVLAEMAGGELGEMSPRLNHTNGARCYGSDGKVSELEGECDGLVSGDGSXKCELEBG	915
Dh	714	YVWITISTESEBEPRAVYTHNGSGYCDGJLIXQDQGGQCDMMKXINDGSLCFRQGV	773
Qy	916	FNCGEPBPLCMYBEGDGCIEPERFRTSIVDGIYTPKXVLOMAYRASHEDKKCEV	975
Dh	774	FNCLDEBRRCYFNHODGVCIEBEFQKTSIKXDCGYTTPGQFLDMASMSVSHQD-QQCGW	832
Qy	976	LVTGER-HSLICTSYHDPDLPNHRPLTGMFPCVASENETQDDRSQEPGSLKKEDEVMILV	1034
Dh	833	VIIQOPASQVCRFTVIDLSEGISQHANYPCTISYRPSQ-----LAQTFFMLRA	881
Qy	1035	CFNRPGERARFIFLTDTGLVRGENOQTVTLXLYLTDVAGSNHSLCTYLSQGNPLINV	1094
Dh	882	YFSQPRMAAAVYHNLVTDTGYGQOKOTTSIVOLDTQSDHGLHNLSCRNNPLIIPV	941
Qy	1095	THQONVLEPHNTSYLNFSPRGVIGISAVALTSTRSIGLSPVNSCISEDEGNHGOQSCIH	1154
Dh	942	VHDSQPRYHQAQVRFSSPLVALISGVALHSPDNFDPYTLSSC-QRGETYSRABQSCVH	1000
Qy	1155	RPCGKODSCPSLLDHDVNVCTSI---GRLMKCAITTCORGRALQASQGYIRPMQ-	1208
Dh	1001	PACRKT-DCELAVAENA-YLNCSSSDRYNG---AQYVSCRTGYVLQIRRDDELIKSGTG	1055
Qy	1209	KEIILITSGSGHWDONVCLPVDGCVPRPSLVYVNFSGSEBTKYKRCISICVPRAKIOG	1268
Dh	1056	PSVVTUTCTEGFMNKQVACERVDCSIRPHNHQVUASFSCEBTEGTGSCSPCRPADOLKG	1115
Qy	1269	LSPLWTLCELDLWMSREYUYSKLECDARPIILANMLYHNCISODNHNVGTICKYCSKGYU	1328
Dh	1116	NNSLITCEBDBMSFPEALCELMCLARPPVADIQTARCKENHKKHSGPCKYUCCKEPYH	1175
Qy	1329	VAESAEGKVNRKLLKIQCEBEGIWEQSGCIPVUCEPERRPVEGMYECTGSPSLDSQCLN	1388
Dh	1176	VPGSSR-KSKRAFKTQCTDQSGMSQEGACSVUTCDPRPKHGLYCTNGHGFQSPSECKIK	1234
Qy	1389	C-----NOBRKRLPLCTKBGLTQOBFKLCENLOQVCEPSPPELNS-VKYUCGQYIGIA	1442
Dh	1235	CEBDBASGGLSANSYHCKDKDTNGNSFVUCSEMGOOC-SVNEINNSMLKQCDPBGVYIGS	1293

QY 1443 VCSPLCVTPEDPMPLENTADLTLEHMEPVKQSTVCGGRORHNDPVLNHCIOSEP 1502
 Db 1234 ECATSCLDHNSSEITLPMNVTRVRIPIHMLNTRERVRVCTGKLNKPIPALIHCVGCEP 1333
 QY 1503 FQADGMDCTINRRAYCHYDGGCCSSTLSKKVLPFAADLDD-ECTCRDPKAEEN 1557
 Db 1354 FMGNVYCAINRRACFVNDGGDCTSTVTKTKVTFPMSCDLQDDACRBDQAEH 1409

Search completed: August 25, 2005, 22:29:44
Job time : 121.721 secs

```
QY      1443 VCSPLCVTPPSDPVMLPBNITADTLEHMMEPVKQSVICTGRQMHPPVLVHCIOGCEP 1502  
Db      1294 ECATSCULDHNSESIIILPMNVTVRDI PHWLNPTRVVRVTAGLKMYPHPALIHCVKGCEP 1353  
QY      1503 FQADGWCDTIINRAYCHYDGGDCSSSTLSKKVI PPAADCOLD-ECTCRDPKABEN 1557  
Db      1354 FMGDNYCDAINNRAFCNTDGGDBCTSTVTKKVTFPMNSCDLGSDCACRDPQAQEH 1409
```

Search completed: August 25, 2005, 22:29:44
Job time : 121.721 secs

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 22:20:46 ; Search time 30 Seconds
(without alignments)
3876.775 Million cell updates/sec

Title: US-09-983-025b-2_COPY_234_1791

Perfect score: 1558
Sequence: 1 SPBESNONGEGSYRAET.....AADCDDECTCRDPKAEENQ 1558

Scoring table: OLIGO

Gapop 60.0 , Gapext 60.0

Searched: 513545 seqs, 74649064 residues

Word size : 5

Total number of hits satisfying chosen parameters: 50545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
- 2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
- 3: /cgn2_6/ptodata/1/1aa/6A.COMB.pep:*
- 4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
- 5: /cgn2_6/ptodata/1/1aa/PTCUS.COMB.pep:*
- 6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	* Query Match	Length	DB ID	Description
1	1303	83.6	1791	4	US-09-827-998-3 Sequence 3, App1
2	1299	83.4	1770	4	US-09-827-998-10 Sequence 10, App1
3	574	36.8	1385	4	US-09-827-998-16 Sequence 16, App1
4	11	0.7	20	4	US-09-827-998-18 Sequence 18, App1
5	9	0.6	211	4	US-09-902-540-13412 Sequence 1412, A
6	8	0.5	47	4	US-09-079-030-90 Sequence 90, App1
7	8	0.5	105	4	US-09-732-210-781 Sequence 781, App1
8	8	0.5	382	4	US-09-949-016-11427 Sequence 11427, A
9	8	0.5	400	4	US-09-252-991A-31900 Sequence 31900, A
10	8	0.5	494	4	US-09-134-000C-4231 Sequence 4231, App
11	8	0.5	592	4	US-09-536-059-3 Sequence 3, App1
12	8	0.5	4536	4	US-09-180-422B-27 Sequence 27, App1
13	8	0.5	4536	4	US-09-079-030-1 Sequence 1, App1
14	8	0.5	4563	4	US-09-108-006C-1 Sequence 1, App1
15	8	0.5	4563	4	US-09-538-092-842 Sequence 842, App
16	7	0.4	18	3	US-08-920-610-4 Sequence 4, App1
17	7	0.4	18	3	US-09-140-149-2 Sequence 2, App1
18	7	0.4	18	3	US-08-672-213-4 Sequence 4, App1
19	7	0.4	18	3	US-08-973-131-21 Sequence 31, App1
20	7	0.4	18	3	US-08-973-131-21 Sequence 31, App1
21	7	0.4	52	4	US-09-615-917-2 Sequence 2, App1
22	7	0.4	61	4	US-09-513-999C-7681 Sequence 7681, App
23	7	0.4	92	4	US-09-540-236-2834 Sequence 2834, App
24	7	0.4	103	4	US-09-107-532A-4945 Sequence 4945, App
25	7	0.4	103	4	US-09-732-210-762 Sequence 762, App
26	7	0.4	103	4	US-09-732-210-763 Sequence 763, App
27	7	0.4	103	4	US-09-732-210-765 Sequence 765, App
			103	4	US-09-732-210-766 Sequence 766, App

28	7	0.4	104	4	US-09-732-210-761 Sequence 761, App
29	7	0.4	104	4	US-09-711-164-323 Sequence 323, App
30	7	0.4	104	4	US-09-492-709A-321 Sequence 321, App
31	7	0.4	107	4	US-09-370-838-113 Sequence 113, App
32	7	0.4	107	4	US-09-854-133-113 Sequence 113, App
33	7	0.4	108	4	US-09-252-991A-21351 Sequence 21351, A
34	7	0.4	113	4	US-09-732-210-774 Sequence 774, App
35	7	0.4	115	4	US-09-732-210-780 Sequence 780, App
36	7	0.4	116	4	US-09-543-681A-7205 Sequence 7205, App
37	7	0.4	118	4	US-09-489-039A-10900 Sequence 10900, A
38	7	0.4	119	4	US-09-270-767-56640 Sequence 56640, A
39	7	0.4	120	4	US-09-248-796A-27858 Sequence 27858, A
40	7	0.4	120	4	US-09-902-540-11618 Sequence 11618, A
41	7	0.4	135	4	US-09-270-767-40611 Sequence 40611, A
42	7	0.4	135	4	US-09-270-767-55827 Sequence 55827, A
43	7	0.4	136	4	US-09-710-279-1852 Sequence 1852, App
44	7	0.4	141	4	US-09-949-016-8944 Sequence 8944, App
45	7	0.4	144	4	US-09-252-991A-16576 Sequence 16576, A

ALIGNMENTS

RESULT 1									
US-09-827-998-3									
Sequence 3, Application US/09827998									
Patent No. 6656700									
GENERAL INFORMATION:									
APPLICANT: Shannon, Mark									
APPLICANT: Gu, Yizhong									
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E									
FILE REFERENCE: MIMMORP-8									
CURRENT APPLICATION NUMBER: US/09/827, 998									
CURRENT FILING DATE: 2001-04-06									
PRIOR APPLICATION NUMBER: US 60/207,456									
PRIOR FILING DATE: 2000-05-26									
PRIOR APPLICATION NUMBER: US 60/236,359									
PRIOR FILING DATE: 2000-09-27									
NUMBER OF SEQ ID NOS: 1881									
SOFTWARE: Acomica Sequence Listing Engine									
Patent No. 6656700									
SEQ ID NO 3									
LENGTH: 1791									
TYPE: PRT									
ORGANISM: Homo sapiens									
US-09-827-998-3									
Query Match									
Best Local Similarity 83.6%; Score 1303; DB 4; Length 1791;									
Matches 1503; Conservative 0; Mismatches 2; Indels 0; Gaps 0;									
QY	1	SPBESNONGEGSYRAETFNSQVGLPIYFGRRRLRLPREVAEIPREAFVEMV	60						
DB	234	SPBESNONGEGSYRAETFNSQVGLPIYFGRRRLRLPREVAEIPREAFVEMV	293						
QY	61	KPBEGQNNPAILIAGVFNCHTYSDDKMAIGISGKXGKGRDARFFSLCTDRYKXATIL	120						
DB	294	KPBEGQNNPAILIAGVFNCHTYSDDKMAIGISGKXGKGRDARFFSLCTDRYKXATIL	353						
QY	121	ISHSRVPGTWTHVAATYDGRHMAIYDGTQVASSLDQSGPLNSPFMAASCRLSLGGDS	180						
DB	354	ISHSRVPGTWTHVAATYDGRHMAIYDGTQVASSLDQSGPLNSPFMAASCRLSLGGDS	413						
QY	181	EDGHYFRGLIGTLVFWSTALPOSHFOHSSQHSQSGEBEATDLVLTSFEPVTEWVPRDE	240						
DB	414	EDGHYFRGLIGTLVFWSTALPOSHFOHSSQHSQSGEBEATDLVLTSFEPVTEWVPRDE	473						
QY	241	KYRLEVLQGFEBEPETLSPLQPLCGQTCVCDNVELISQYNGVWPLRGEKVIYQVNNIC	300						
DB	474	KYRLEVLQGFEBEPETLSPLQPLCGQTCVCDNVELISQYNGVWPLRGEKVIYQVNNIC	533						
QY	301	DDEGLNPVEEEOIRLOHEALNEAFSRYNISWOLSVHYQVNSTLRHRVVLVNCPSKIGN	360						

534 DDEGLNPVSEBQIRLQHEALNEAFSRYNISWQLSVHQNSTLRHRVVLVNCESPCKIGN 593
QY |||||
361 DHCPECEHPLTGYDGGDCRLQGRCSWNRBDGLCHVECNMMLNDPDDGCCDPQVADVR 420
DB |||||
594 DHCPECEHPLTGYDGGDCRLQGRCSWNRBDGLCHVECNMMLNDPDDGCCDPQVADVR 653
QY KTCFDPDSPKAYMSVKEALKEALQLNSTHPLNITYFASSVREDLAAGATWPMKDAVTHLG 480
DB KTCFDPDSPKAYMSVKEALKEALQLNSTHPLNITYFASSVREDLAAGATWPMKDAVTHLG 713
QY 481 GIVLSPAYYGMGPHDTMTIHEVHVLGLYHVFKGVSERESCNDCKETVPSMETGDLCAD 540
DB GIVLSPAYYGMGPHDTMTIHEVHVLGLYHVFKGVSERESCNDCKETVPSMETGDLCAD 773
QY 541 TAPPKSELCEBEPRTDTCGFTFPGAPFTNMSYTDNCTDFTPQVARMHCYIDL 600
DB TAPPKSELCEBEPRTDTCGFTFPGAPFTNMSYTDNCTDFTPQVARMHCYIDL 833
QY 601 YQWTEBARKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCACTEDGTFROY 660
DB YQWTEBARKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCACTEDGTFROY 893
QY 834 YQWTEBARKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCACTEDGTFROY 893
DB YQWTEBARKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCACTEDGTFROY 953
QY 661 VHTASSRRVCDSSGYWTPBEAVBPVDVQPCPSLQAMSPREVLHYHMMVPCPTGCSL 720
DB VHTASSRRVCDSSGYWTPBEAVBPVDVQPCPSLQAMSPREVLHYHMMVPCPTGCSL 953
QY 721 ELFPQHVQADTLTLMWTSFPMESSQVLFDTIELLENKESHLDLPDTCIPLITIKLHV 780
DB ELFPQHVQADTLTLMWTSFPMESSQVLFDTIELLENKESHLDLPDTCIPLITIKLHV 1013
QY 954 ELFPQHVQADTLTLMWTSFPMESSQVLFDTIELLENKESHLDLPDTCIPLITIKLHV 1013
DB ELFPQHVQADTLTLMWTSFPMESSQVLFDTIELLENKESHLDLPDTCIPLITIKLHV 1013
QY 781 DGKYSGVKVVYTFDERIEIDALLTSOPHSPLCSGCRPRVYOVLRDPPFASGLPVVYVTHSH 840
DB DGKYSGVKVVYTFDERIEIDALLTSOPHSPLCSGCRPRVYOVLRDPPFASGLPVVYVTHSH 1014
QY 1014 DGKYSGVKVVYTFDERIEIDALLTSOPHSPLCSGCRPRVYOVLRDPPFASGLPVVYVTHSH 1073
DB DGKYSGVKVVYTFDERIEIDALLTSOPHSPLCSGCRPRVYOVLRDPPFASGLPVVYVTHSH 1073
QY 841 RKFTDVEVTPGQMYOYOVLAAGELGASPLNHIHGAFCGDKGYSERLGEEDCDGDL 900
DB RKFTDVEVTPGQMYOYOVLAAGELGASPLNHIHGAFCGDKGYSERLGEEDCDGDL 1133
QY 1074 RKFTDVEVTPGQMYOYOVLAAGELGASPLNHIHGAFCGDKGYSERLGEEDCDGDL 1133
DB RKFTDVEVTPGQMYOYOVLAAGELGASPLNHIHGAFCGDKGYSERLGEEDCDGDL 1133
QY 901 VSGGCKVCELEBEGFNCVGBPSLCMYEEDGICEPBERKTSIYDCCGYTPPKGLDOWAT 960
DB VSGGCKVCELEBEGFNCVGBPSLCMYEEDGICEPBERKTSIYDCCGYTPPKGLDOWAT 1134
QY 1134 VSGGCKVCELEBEGFNCVGBPSLCMYEEDGICEPBERKTSIYDCCGYTPPKGLDOWAT 1193
DB VSGGCKVCELEBEGFNCVGBPSLCMYEEDGICEPBERKTSIYDCCGYTPPKGLDOWAT 1193
QY 961 RAYSHSHDKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETODRSEOP 1020
DB RAYSHSHDKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETODRSEOP 1253
QY 1194 RAYSHSHDKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETODRSEOP 1253
DB RAYSHSHDKKCPVSLVTGEPHSLICTSYHBDLPNHRPLTGMFPCVASENETODRSEOP 1253
QY 1021 EGSIKKEDVWLKVCENRPGBARAIFLFTTDLGVPSGHQPTVTLVTLTVRGSNHSLSGT 1080
DB EGSIKKEDVWLKVCENRPGBARAIFLFTTDLGVPSGHQPTVTLVTLTVRGSNHSLSGT 1313
QY 1254 EGSIKKEDVWLKVCENRPGBARAIFLFTTDLGVPSGHQPTVTLVTLTVRGSNHSLSGT 1313
DB EGSIKKEDVWLKVCENRPGBARAIFLFTTDLGVPSGHQPTVTLVTLTVRGSNHSLSGT 1313
QY 1081 YGLSCQHNPLINTHTHQNVLPHHTTSVLANFSSPRVIGISAVALARTSSRTGLSAPNSCIS 1140
DB YGLSCQHNPLINTHTHQNVLPHHTTSVLANFSSPRVIGISAVALARTSSRTGLSAPNSCIS 1314
QY 1314 YGLSCQHNPLINTHTHQNVLPHHTTSVLANFSSPRVIGISAVALARTSSRTGLSAPNSCIS 1373
DB YGLSCQHNPLINTHTHQNVLPHHTTSVLANFSSPRVIGISAVALARTSSRTGLSAPNSCIS 1373
QY 1141 EDEBQNHQGSCHIRPCGKODSCPSLLLDHADVNCISIGBLMKCAITCORGALQASS 1200
DB EDEBQNHQGSCHIRPCGKODSCPSLLLDHADVNCISIGBLMKCAITCORGALQASS 1433
QY 1374 EDEBQNHQGSCHIRPCGKODSCPSLLLDHADVNCISIGBLMKCAITCORGALQASS 1433
DB EDEBQNHQGSCHIRPCGKODSCPSLLLDHADVNCISIGBLMKCAITCORGALQASS 1433
QY 1201 GQYIRPMQKEILLTCSSGMDQWNSCLPVDGVDPSPVLVNYANFSCSEGTFLKRCISIC 1260
DB GQYIRPMQKEILLTCSSGMDQWNSCLPVDGVDPSPVLVNYANFSCSEGTFLKRCISIC 1434
QY 1434 GQYIRPMQKEILLTCSSGMDQWNSCLPVDGVDPSPVLVNYANFSCSEGTFLKRCISIC 1493
DB GQYIRPMQKEILLTCSSGMDQWNSCLPVDGVDPSPVLVNYANFSCSEGTFLKRCISIC 1493
QY 1261 VPPAKLOGLSTWLTCLBDGLMSLPBYVCKLECDAPPIILNANLILPHCLQDNHDVGTIC 1320
DB VPPAKLOGLSTWLTCLBDGLMSLPBYVCKLECDAPPIILNANLILPHCLQDNHDVGTIC 1553
QY 1494 VPPAKLOGLSTWLTCLBDGLMSLPBYVCKLECDAPPIILNANLILPHCLQDNHDVGTIC 1553
DB VPPAKLOGLSTWLTCLBDGLMSLPBYVCKLECDAPPIILNANLILPHCLQDNHDVGTIC 1553
QY 1321 YBCKPGYVVASAAGKRNKLKLCQLEGGIWEQSGCIPVVCBPPPVFREGMYCTNGFS 1380
DB YBCKPGYVVASAAGKRNKLKLCQLEGGIWEQSGCIPVVCBPPPVFREGMYCTNGFS 1613
QY 1554 YBCKPGYVVASAAGKRNKLKLCQLEGGIWEQSGCIPVVCBPPPVFREGMYCTNGFS 1613
DB YBCKPGYVVASAAGKRNKLKLCQLEGGIWEQSGCIPVVCBPPPVFREGMYCTNGFS 1613
QY 1381 LDSQCVLNCNQBREKPLICTKEGLMTQEFKLCENTQGECPRPSPSELNSVEYKCEQGYGI 1440
DB LDSQCVLNCNQBREKPLICTKEGLMTQEFKLCENTQGECPRPSPSELNSVEYKCEQGYGI 1614
QY 1614 LDSQCVLNCNQBREKPLICTKEGLMTQEFKLCENTQGECPRPSPSELNSVEYKCEQGYGI 1673
DB LDSQCVLNCNQBREKPLICTKEGLMTQEFKLCENTQGECPRPSPSELNSVEYKCEQGYGI 1673

QY 1441 GAVCSPLCVIPSPDPVVLNENITADTLEHMMEPVKVQSIYCTGRQWHPVVLVNCISQSC 1500
DB 1674 GAVCSPLCVIPSPDPVVLNENITADTLEHMMEPVKVQSIYCTGRQWHPVVLVNCISQSC 1733
QY 1501 EPFOA 1505
DB 1734 EPFOA 1738
RESULT 2
US-09-827-998-10
; Sequence 10, Application US/09827998
; Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecmics Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 10
; LENGTH: 1770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-10
Query Match 83.4%; Score 1299; DB 4; Length 1770;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 1 SPEESNONGESYEAETFNQVGLPILYFSGRERILLRBYLAETPREAFTVAMV 60
DB 234 SPEESNONGESYEAETFNQVGLPILYFSGRERILLRBYLAETPREAFTVAMV 293
QY 61 KPEGGQNNPAILIGVFNDCSHTVSDKGWALGIRSGDKGRDARFFSLCTDRVKATIL 120
DB 294 KPEGGQNNPAILIGVFNDCSHTVSDKGWALGIRSGDKGRDARFFSLCTDRVKATIL 353
QY 121 ISHSRYQPTGTHVAATYDGRHVALYVDGTQVASSLDQSGPLNSPMAACRSILLGSDS 180
DB 354 ISHSRYQPTGTHVAATYDGRHVALYVDGTQVASSLDQSGPLNSPMAACRSILLGSDS 413
QY 181 EDGHYRGRGHGTLVFWSTALPOSHPOHSSQHSSEBEATDVLVTASPEPVNTEWPRDE 240
DB 414 EDGHYRGRGHGTLVFWSTALPOSHPOHSSQHSSEBEATDVLVTASPEPVNTEWPRDE 473
QY 241 KYRLEVLQGFEBEPILSLPRLCGQTVCDNVELISQYNGYWPRLRGEKVIROYVNIC 300
DB 474 KYRLEVLQGFEBEPILSLPRLCGQTVCDNVELISQYNGYWPRLRGEKVIROYVNIC 533
QY 301 DDEGLNPVSEBQIRLQHEALNEAFSRYNISWQLSVHQNSTLRHRVVLVNCESPCKIGN 360
DB 534 DDEGLNPVSEBQIRLQHEALNEAFSRYNISWQLSVHQNSTLRHRVVLVNCESPCKIGN 593
QY 361 DHCPECEHPLTGYDGGDCRLQGRCSWNRBDGLCHVECNMMLNDPDDGCCDPQVADVR 420
DB 594 DHCPECEHPLTGYDGGDCRLQGRCSWNRBDGLCHVECNMMLNDPDDGCCDPQVADVR 653
QY 421 KTCFDPDSPKAYMSVKEALKEALQLNSTHPLNITYFASSVREDLAAGATWPMKDAVTHLG 480
DB 654 KTCFDPDSPKAYMSVKEALKEALQLNSTHPLNITYFASSVREDLAAGATWPMKDAVTHLG 713
QY 481 GIVLSPAYYGMGPHDTMTIHEVHVLGLYHVFKGVSERESCNDCKETVPSMETGDLCAD 540
DB 714 GIVLSPAYYGMGPHDTMTIHEVHVLGLYHVFKGVSERESCNDCKETVPSMETGDLCAD 773

QY 541 TAPTKSELCEBEPSTDTGFTFPGAPFTNMSYTDNDCTDNTFNOVARMHCYDLV 600
DB 774 TAPTKSELCEBEPSTDTGFTFPGAPFTNMSYTDNDCTDNTFNOVARMHCYDLV 833
QY 601 YQWTESSRKPTPIPIPMVIGQTNKSLTIHMLPPISGVVYDRASGSLCGACTEBGTFRQY 660
DB 834 YQWTESSRKPTPIPIPMVIGQTNKSLTIHMLPPISGVVYDRASGSLCGACTEBGTFRQY 893
QY 661 VHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSILOAMSPEVHL YHMMTVPCPTGCSL 720
DB 894 VHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSILOAMSPEVHL YHMMTVPCPTGCSL 953
QY 721 ELLEFQHVQADTLTLMTWTSFPMSSOVLFTTEILLENKESVHLGPDLCIDIPLTIKLVH 780
DB 954 ELLEFQHVQADTLTLMTWTSFPMSSOVLFTTEILLENKESVHLGPDLCIDIPLTIKLVH 1013
QY 781 DGKVSQVYVTFPDRERIEIDALLTSQPHSPICSGCRPVRYQVLRDPPFASGLPVVVTSH 840
DB 1014 DGKVSQVYVTFPDRERIEIDALLTSQPHSPICSGCRPVRYQVLRDPPFASGLPVVVTSH 1073
QY 841 RKFTDVEVTPGQMYQYQVLAEGELGEASPLNHIHGAPYCGDGKVSERLGEBCDDGL 900
DB 1074 RKFTDVEVTPGQMYQYQVLAEGELGEASPLNHIHGAPYCGDGKVSERLGEBCDDGL 1133
QY 901 VSGDGSCKVCELEBGFNCVGPBSLCYMYEGDICEPFRKTSIYDCCGYTPKGYLDQMAT 960
DB 1134 VSGDGSCKVCELEBGFNCVGPBSLCYMYEGDICEPFRKTSIYDCCGYTPKGYLDQMAT 1193
QY 961 RAYSSHEDKKCPISLVTEBPHSLICTSYHBDLPNHRPLTGMPPCVASENETODDRSEOP 1020
DB 1194 RAYSSHEDKKCPISLVTEBPHSLICTSYHBDLPNHRPLTGMPPCVASENETODDRSEOP 1253
QY 1021 EGSILKKEDEWMLKVCENRPGESARAIFILTTDGLVPGEHQPTVTLVLTIDVRSNHSIGT 1080
DB 1254 EGSILKKEDEWMLKVCENRPGESARAIFILTTDGLVPGEHQPTVTLVLTIDVRSNHSIGT 1313
QY 1081 YGLSCQHNPLIINTVTHQNVLFHHTTSVILNFPSSPRVIGISAVARTSRIQLSAPNSCIS 1140
DB 1314 YGLSCQHNPLIINTVTHQNVLFHHTTSVILNFPSSPRVIGISAVARTSRIQLSAPNSCIS 1373
QY 1141 EDEGQNHQGSCHIRPGCKODSCPSLLLDHADVNTCSIGPGLMKCAITTCQRFALQAS 1200
DB 1374 EDEGQNHQGSCHIRPGCKODSCPSLLLDHADVNTCSIGPGLMKCAITTCQRFALQAS 1433
QY 1201 GQYIRPMQKEILLTCSSGHMDQNVSCLPVDCGVDPBSLVNANFSCSEGTFLKRCISIC 1260
DB 1434 GQYIRPMQKEILLTCSSGHMDQNVSCLPVDCGVDPBSLVNANFSCSEGTFLKRCISIC 1493
QY 1261 VPPAKLOGLSFWLTCLBDGLMSLEPVYCKLECDAPRIITLNNALLPCLQDNDHVTGTC 1320
DB 1494 VPPAKLOGLSFWLTCLBDGLMSLEPVYCKLECDAPRIITLNNALLPCLQDNDHVTGTC 1553
QY 1321 YECRPGYVVAESASGKVRNKLKIQCLEGGIWEQSGCIPVCEBPPPVFBEMVCTNGFS 1380
DB 1554 YECRPGYVVAESASGKVRNKLKIQCLEGGIWEQSGCIPVCEBPPPVFBEMVCTNGFS 1613
QY 1381 LDSQCVLNCQERKEPILCTKEGLMTQBFKLCENLQGECPRPSELSNVEYKCEQGYGI 1440
DB 1614 LDSQCVLNCQERKEPILCTKEGLMTQBFKLCENLQGECPRPSELSNVEYKCEQGYGI 1673
QY 1441 GAVSPLCLVTPSPVWMLPENITADTLEHMMEPYKQSVICTGRQWHPDPVVLVHCIOQC 1500
DB 1674 GAVSPLCLVTPSPVWMLPENITADTLEHMMEPYKQSVICTGRQWHPDPVVLVHCIOQC 1733
QY 1501 E 1501
DB 1734 E 1734

RESULT 3
US-09-827-998-16
; Sequence 16, Application US/09827998

Patent No. 6656700
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: NMH0RF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aeomica Sequence Listing Engine
; Patent No. 6656700
; SEQ ID NO 16
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-16

Query Match 36.8%; Score 574; DB 4; Length 1385;
Best Local Similarity 99.5%; Pred. No. 0;
Matches 1074; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

QY 480 GGIVLSAYVGMPEHTDTMTHEVGHVULGLVHFVGVSEBSCNDPCKETVPSMETGDLCA 539
DB 307 GGIVLSAYVGMPEHTDTMTHEVGHVULGLVHFVGVSEBSCNDPCKETVPSMETGDLCA 366
QY 540 DTAPTPSELCEBEPSTDTGFTFPGAPFTNMSYTDNDCTDNTFNOVARMHCYDLV 599
DB 367 DTAPTPSELCEBEPSTDTGFTFPGAPFTNMSYTDNDCTDNTFNOVARMHCYDLV 426
QY 600 YQWTESSRKPTPIPIPMVIGQTNKSLTIHMLPPISGVVYDRASGSLCGACTEBGTFRQ 659
DB 427 YQWTESSRKPTPIPIPMVIGQTNKSLTIHMLPPISGVVYDRASGSLCGACTEBGTFRQ 486
QY 660 YHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSILOAMSPEVHL YHMMTVPCPTGCS 719
DB 487 YHTASSRRVCDSSGYWTPBEAVGPDPVDQPCPSILOAMSPEVHL YHMMTVPCPTGCS 546
QY 720 ELLEFQHVQADTLTLMTWTSFPMSSOVLFTTEILLENKESVHLGPDLCIDIPLTIKLVH 779
DB 547 ELLEFQHVQADTLTLMTWTSFPMSSOVLFTTEILLENKESVHLGPDLCIDIPLTIKLVH 606
QY 780 VDGKVSQVYVTFPDRERIEIDALLTSQPHSPICSGCRPVRYQVLRDPPFASGLPVVVTSH 839
DB 607 VDGKVSQVYVTFPDRERIEIDALLTSQPHSPICSGCRPVRYQVLRDPPFASGLPVVVTSH 666
QY 840 HRKFTDVEVTPGQMYQYQVLAEGELGEASPLNHIHGAPYCGDGKVSERLGEBCDDGD 899
DB 667 HRKFTDVEVTPGQMYQYQVLAEGELGEASPLNHIHGAPYCGDGKVSERLGEBCDDGD 726
QY 900 LVSQDGSCKVCELEBGFNCVGPBSLCYMYEGDICEPFRKTSIYDCCGYTPKGYLDQMA 959
DB 727 LVSQDGSCKVCELEBGFNCVGPBSLCYMYEGDICEPFRKTSIYDCCGYTPKGYLDQMA 786
QY 960 TRAYSSHEDKKCPISLVTEBPHSLICTSYHBDLPNHRPLTGMPPCVASENETODDRSEQ 1019
DB 787 TRAYSSHEDKKCPISLVTEBPHSLICTSYHBDLPNHRPLTGMPPCVASENETODDRSEQ 846
QY 1020 PEGSLKKEDEWMLKVCENRPGESARAIFILTTDGLVPGEHQPTVTLVLTIDVRSNHSIG 1079
DB 847 PEGSLKKEDEWMLKVCENRPGESARAIFILTTDGLVPGEHQPTVTLVLTIDVRSNHSIG 906
QY 1080 TYGLSCQHNPLIINTVTHQNVLFHHTTSVILNFPSSPRVIGISAVARTSRIQLSAPNSCI 1139
DB 907 TYGLSCQHNPLIINTVTHQNVLFHHTTSVILNFPSSPRVIGISAVARTSRIQLSAPNSCI 966
QY 1140 SEDEGQNHQGSCHIRPGCKODSCPSLLLDHADVNTCSIGPGLMKCAITTCQRFALQAS 1199
DB 967 SEDEGQNHQGSCHIRPGCKODSCPSLLLDHADVNTCSIGPGLMKCAITTCQRFALQAS 1026

Qy	1200	SGOYIRPMOKIILLTSSGSHNDONVSLCPVQCGVDPDLVNYANSCEGKFLKRGIS	1259
Db	1027	SEQYIRLMQKEIILLTSSGSHNDONVSLCPVQCGVDPDLVNYANFSCGKFLKRGIS	10866
Qy	1260	CVPPAKIOGSLPMLTCLBEGJMSLPEVYCKLECDAPRIILNANLILPHCLDNHDVGTIC	13119
Db	1087	CVPPAKIOGSLPMLTCLBEGJMSLPEVYCKLECDAPRIILNANLILPHCLDNHDVGTIC	11466
Qy	1320	KYEKPCGYVVAESAAGKVRNLLIKIOCLEGGIWEQSGCIPVYCEPPRVFEGMETCTNGF	13797
Db	1147	KYEKPCGYVVAESAAGKVRNLLIKIOCLEGGIWEQSGCIPVYCEPPRVFEGMETCTNGF	12060
Qy	1380	SLDSQCVLNCQOEERKPIILCTKGLMWOERKLCENLOGEPPRPSLSNSTYUCSGQYG	14339
Db	1207	SLDSQCVLNCQOEERKPIILCTKGLMWOERKLCENLOGECPRPSELSNSTYUCSGQYG	12666
Qy	1440	IGAVCSPLCVIPSPDPVMLPENITADTLLEHMMBPVKQSIYCTGGRQWHPVPLVHICIS	14999
Db	1267	IGAVCSPLCVIPSPDPVMLPENITADTLLEHMMBPVKQSIYCTGGRQWHPVPLVHICIS	13266
Qy	1500	CEPPADQMGCTINNRACVHYDGGDCSSSTLSKKVIRPADCDLDECTCGDPPAEANQ	1558
Db	1327	CEPPADQMGCTINNRACVHYDGGDCSSSTLSKKVIRPADCDLDECTCGDPPAEANQ	1385

```

RESULT 4
US-09-827-998-18
Sequence 18, Application US/09827998
Patent No. 6656700
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: MPMORF-8
CURRENT APPLICATION NUMBER: US/09/827,998
CURRENT FILING DATE: 2001-04-06
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 66/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aecomia Sequence Listing Engine
Patent No. 6656700
SEQ ID NO 18
LENGTH: 20
TYPE: PRT
ORGANISM: Homo sapiens
US-09-827-998-18

Query Match          0.7%; Score 11; DB 4; Length 20;
Best Local Similarity 100.0%; Pred. No. 0.0032;
Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps

QY          480 GGIVLSPAYYG 490
          |||||
Db          10 GGIVLSPAYYG 20

RESULT 5
US-09-902-540-13412
Sequence 13412, Application US/09902540
Patent No. 6833447
GENERAL INFORMATION:
APPLICANT: Goldman, Barry S.
APPLICANT: Hinkle, Gregory J.
APPLICANT: Slater, Steven C.
APPLICANT: Wiegand, Roger C.
TITLE OF INVENTION: Myxococcus xanthus Genome Sequences and Uses Thereof
FILE REFERENCE: 38-10(15849)B
CURRENT APPLICATION NUMBER: US/09/902,540
CURRENT FILING DATE: 2001-07-10
PRIOR APPLICATION NUMBER: 60/217,883
PRIOR FILING DATE: 2000-07-10

```

```

; NUMBER OF SEQ ID NOS: 16825
; SEQ ID NO 13412
; LENGTH: 211
; TYPE: PRF
; ORGANISM: Myxococcus xanthus
US-09-902-540-13412

Query Match          0.6%; Score 9; DB 4; Length 211;
Best Local Similarity 100.0%; Pred. No. 2.8;
Matches 9; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      500 HEVGHVTLGL 508
      |||||
Db      23 HEVGHVTLGL 31

```

```

RESULT 6
US-09-079-030-90
; Sequence 90, Application US/09079030
; Patent No. 6635623
; GENERAL INFORMATION:
; APPLICANT: Guevera, Jr., Juan G.
; APPLICANT: Hoogveen, Ron C.
; APPLICANT: Moore, Paul J.
; TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
; TITLE OF INVENTION: VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
; NUMBER OF SEQUENCES: 229
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Arnold, White & Durkee
; STREET: P.O. Box 4433
; CITY: Houston
; STATE: Texas
; COUNTRY: USA
; ZIP: 77210
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/079,030
; FILING DATE: Concurrently Herewith
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: McMillian, Nabeeja R.
; REGISTRATION NUMBER: P-43,363
; REFERENCE/DOCKET NUMBER: ARAG:003
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 512/418-3000
; TELEFAX: 512/474-7577
; INFORMATION FOR SEQ ID NO: 90:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 47 amino acids
; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; US-09-079-030-90

Query Match 0.5%; Score 8; DB 4; Length 47;
Best Local Similarity 100.0%; Pred. No. 7.1;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Oy 1079 GTYGLSCQ 1086
|||
|||
|||
Db 32 GTYGLSCQ 39

RESULT 7
US-09-732-210-781
; Sequence 781, Application US/09732210
; Patent No. 6573361
; GENERAL INFORMATION:
; APPLICANT: Bunkers, Greg J.

```

```

; APPLICANT: Liang, Jihong
; APPLICANT: Mitranck, Cindy A.
; APPLICANT: Seale, Jeffrey W.
; APPLICANT: Wu, Yonnie S.
; TITLE OF INVENTION: Anti-fungal Proteins and Methods for Their Use
; FILE REFERENCE: 38-21(15036)B
; CURRENT APPLICATION NUMBER: US/09/732,210
; CURRENT FILING DATE: 2000-12-07
; PRIOR APPLICATION NUMBER: US 60/169,513
; PRIOR FILING DATE: 1999-12-07
; PRIOR APPLICATION NUMBER: US 60/169,340
; PRIOR FILING DATE: 1999-12-07
; NUMBER OF SEQ ID NOS: 1753
; SEQ ID NO 781
; LENGTH: 105
; TYPE: PRT
; ORGANISM: Thermotoga maritima
US-09-732-210-781

```

```

Query Match      0.5%; Score 8; DB 4; Length 105;
Best Local Similarity 100.0%; Pred. No. 15;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      94 SGKDKGR 101
Db      13 SGKDKGR 20

```

```

RESULT 8
; Sequence 11427, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; FILE REFERENCE: C1001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 11427
; LENGTH: 382
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-11427

```

```

Query Match      0.5%; Score 8; DB 4; Length 382;
Best Local Similarity 100.0%; Pred. No. 48;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      436 VKELKAL 443
Db      40 VKELKAL 47

```

```

RESULT 9
US-09-252-991A-31900
; Sequence 31900, Application US/09252991A
; Patent No. 6551795
; GENERAL INFORMATION:
; APPLICANT: Marc J. Rubenfield et al.
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO PSEUDOMONAS
; FILE REFERENCE: 107196.136
; CURRENT APPLICATION NUMBER: US/09/252,991A
; CURRENT FILING DATE: 1999-02-18

```

```

; PRIOR APPLICATION NUMBER: US 60/074,788
; PRIOR FILING DATE: 1998-02-18
; PRIOR APPLICATION NUMBER: US 60/094,190
; PRIOR FILING DATE: 1998-07-27
; NUMBER OF SEQ ID NOS: 33142
; SEQ ID NO 31900
; LENGTH: 400
; TYPE: PRT
; ORGANISM: Pseudomonas aeruginosa
US-09-252-991A-31900

```

```

Query Match      0.5%; Score 8; DB 4; Length 400;
Best Local Similarity 100.0%; Pred. No. 50;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      45 VLAEIPRE 52
Db      189 VLAEIPRE 196

```

```

RESULT 10
US-09-134-000C-4291
; Sequence 4291, Application US/09134000C
; Patent No. 6617156
; GENERAL INFORMATION:
; APPLICANT: Lynn Doucette-Stamm et al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO
; FILE REFERENCE: 032796-032
; CURRENT APPLICATION NUMBER: US/09/134,000C
; CURRENT FILING DATE: 1998-08-13
; PRIOR APPLICATION NUMBER: US 60/055,778
; PRIOR FILING DATE: 1997-08-15
; NUMBER OF SEQ ID NOS: 6812
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 4291
; LENGTH: 484
; TYPE: PRT
; ORGANISM: Enterococcus faecalis
US-09-134-000C-4291

```

```

Query Match      0.5%; Score 8; DB 4; Length 494;
Best Local Similarity 100.0%; Pred. No. 61;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

Qy      646 SLGACCTE 653
Db      368 SLGACCTE 375

```

```

RESULT 11
US-09-536-059-3
; Sequence 3, Application US/09536059
; Patent No. 6544737
; GENERAL INFORMATION:
; APPLICANT: Blumenfeld, Martha
; APPLICANT: Chumakov, Ilya
; APPLICANT: Bougueleret, Lydie
; APPLICANT: Cohen-Akenine, Amick
; TITLE OF INVENTION: GENOMIC SEQUENCE OF THE purH GENE AND purH-RELATED BIALLERIC
; FILE REFERENCE: GENSET.0584US
; CURRENT APPLICATION NUMBER: US/09/536,059
; CURRENT FILING DATE: 2000-03-31
; PRIOR APPLICATION NUMBER: US 60/125,961
; PRIOR FILING DATE: 1999-03-24
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: Patent.pm
; SEQ ID NO 3
; LENGTH: 592
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:

```

NAME/KEY: VARIANT
LOCATION: 116
OTHER INFORMATION: Xaa-thr or Ser
US-09-536-059-3

Query Match 0.5%; Score 8; DB 4; Length 592;
Best Local Similarity 100.0%; Pred. No. 71;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 436 VKELKEAL 443
DB 250 VKELKEAL 257

RESULT 12
US-09-180-422B-27
Sequence 27, Application US/09180422B
Patent No. 6444644
GENERAL INFORMATION:

APPLICANT: BRUCKDORFER, KARL R
ETTELDAIE, CAMILLE
TITLE OF INVENTION: ANTICOAGULANT PEPTIDE FRAGMENTS DERIVED
FROM APOLOPROTEIN B-100

NUMBER OF SEQUENCES: 27
CORRESPONDENCE ADDRESS:
ADDRESSEE: NIXON & VANDERHAYE, P.C.
STREET: 1100 NORTH GLEBE ROAD, 8TH FLOOR
CITY: ARLINGTON
STATE: VA
COUNTRY: USA
ZIP: 22201

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
OPERATING SYSTEM: IBM PC compatible
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/180,422B
FILING DATE: 07-Dec-1998
CLASSIFICATION: <Unknown>
ATTORNEY/AGENT INFORMATION:
NAME: SADOFF, B.J.
REGISTRATION NUMBER: 36663
REFERENCE/DOCKET NUMBER: 117-268
TELECOMMUNICATION INFORMATION:
TELEPHONE: 7038164000
TELEFAX: 7038164100

INFORMATION FOR SEQ ID NO: 27:

SEQUENCE CHARACTERISTICS:
LENGTH: 4536 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 27:
US-09-180-422B-27

Query Match 0.5%; Score 8; DB 4; Length 4536;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1079 GTYGLSCQ 1086
DB 1472 GTYGLSCQ 1479

RESULT 13
US-09-079-030-1
Sequence 1, Application US/09079030
Patent No. 6635623
GENERAL INFORMATION:
APPLICANT: Guevera, Jr., Juan G.
APPLICANT: Hoogeven, Ron C.

APPLICANT: Moore, Paul J.
TITLE OF INVENTION: LIPOPROTEINS AS NUCLEIC ACID DELIVERY
VECTORS FOR TRANSFECTION OF EUKARYOTIC CELLS
NUMBER OF SEQUENCES: 229
CORRESPONDENCE ADDRESS:
ADDRESSEE: Arnold, White & Durkee
STREET: P.O. Box 4433
CITY: Houston
STATE: Texas
COUNTRY: USA
ZIP: 77210

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,030
FILING DATE: Concurrently Herewith
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: McMillian, Nabeela R.
REGISTRATION NUMBER: P-43,363
REFERENCE/DOCKET NUMBER: ARAG:003
TELECOMMUNICATION INFORMATION:
TELEPHONE: 512/418-3000
TELEFAX: 512/474-7577

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4536 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
US-09-079-030-1

Query Match 0.5%; Score 8; DB 4; Length 4536;
Best Local Similarity 100.0%; Pred. No. 4.5e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1079 GTYGLSCQ 1086
DB 1472 GTYGLSCQ 1479

RESULT 14
US-09-108-006C-1
Sequence 1, Application US/09108006C
Patent No. 6524613
GENERAL INFORMATION:

APPLICANT: Steer, Clifford J.
Kren, Betsy T.
Bandyopadhyay, Paramita
Roy-Chowdhury, Jayanta
TITLE OF INVENTION: Hepatocellular Chimeraplasty
NUMBER OF SEQUENCES: 62
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kimeragen, Inc.
STREET: 300 Pheasant Run
CITY: Newtown
STATE: PA
COUNTRY: USA
ZIP: 18940

COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSeq for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/108,006C
FILING DATE: 30-Jun-1992
CLASSIFICATION: <Unknown>
PRIOR APPLICATION NUMBER: 60/054,288

Job time : 33 secs

FILING DATE: 30-APR-1997
APPLICATION NUMBER: 60/054,837
FILING DATE: 05-AUG-1997
APPLICATION NUMBER: 60/064,996
FILING DATE: 10-NOV-1997
APPLICATION NUMBER: 60/074,497
FILING DATE: 12-FEB-1998
APPLICATION NUMBER: PCT US 98/08834
FILING DATE: 30-APR-1998
ATTORNEY/AGENT INFORMATION:
NAME: Friebe, Thomas
REGISTRATION NUMBER: 29258
REFERENCE/DOCKET NUMBER: 7991-015-999
TELECOMMUNICATION INFORMATION:
TELEPHONE: 215-504-4444
TELEFAX: 215-504-4545
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 4563 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-108-006C-1

Query Match 0.5%; Score 8; DB 4; Length 4563;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1079 GTYGLSCQ 1086
Db 1499 GTYGLSCQ 1506

RESULT 15
US-09-538-092-842
Sequence 842, Application US/09538092
Patent No. 6753314
GENERAL INFORMATION:
APPLICANT: Gile, Lois
TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
FILE REFERENCE: 15966-542
CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
SOFTWARE: CurapatSeqFormatter Version 0.9
SEQ ID NO 842
LENGTH: 4563
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc feature
LOCATION: (0)..(0)
OTHER INFORMATION: Polypeptide Accession Number P04114
US-09-538-092-842

Query Match 0.5%; Score 8; DB 4; Length 4563;
Best Local Similarity 100.0%; Pred. No. 4.6e+02;
Matches 8; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1079 GTYGLSCQ 1086
Db 1499 GTYGLSCQ 1506

Search completed: August 25, 2005, 22:29:58

This Page Blank (uspto)

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 25, 2005, 22:21:31 ; Search time 116 Seconds

(without alignments)
5277.405 Million cell updates/sec

Title: US-09-983-025B-2_COPY_234_1791
Perfect score: 1558
Sequence: 1 SPPESSNQNGEGSYREAF.....AADCDLDECTCRDPKAEENQ 1558

Scoring table:
Gapop 60.0 , Gapext 60.0

Searched: 1767149 seqs, 392926209 residues

Word size : 5

Total number of hits satisfying chosen parameters: 233670

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Listing first 45 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/ptodata/2/pubppaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/2/pubppaa/PCRT_NEW_PUB.pep.*
- 3: /cgn2_6/ptodata/2/pubppaa/US06_NEW_PUB.pep.*
- 4: /cgn2_6/ptodata/2/pubppaa/US06_PUBCOMB.pep.*
- 5: /cgn2_6/ptodata/2/pubppaa/US07_NEW_PUB.pep.*
- 6: /cgn2_6/ptodata/2/pubppaa/PCRTUS_PUBCOMB.pep.*
- 7: /cgn2_6/ptodata/2/pubppaa/US08_NEW_PUB.pep.*
- 8: /cgn2_6/ptodata/2/pubppaa/US08_PUBCOMB.pep.*
- 9: /cgn2_6/ptodata/2/pubppaa/US09A_PUBCOMB.pep.*
- 10: /cgn2_6/ptodata/2/pubppaa/US09B_PUBCOMB.pep.*
- 11: /cgn2_6/ptodata/2/pubppaa/US09C_PUBCOMB.pep.*
- 12: /cgn2_6/ptodata/2/pubppaa/US09C_NEW_PUB.pep.*
- 13: /cgn2_6/ptodata/2/pubppaa/US10A_PUBCOMB.pep.*
- 14: /cgn2_6/ptodata/2/pubppaa/US10B_PUBCOMB.pep.*
- 15: /cgn2_6/ptodata/2/pubppaa/US10C_PUBCOMB.pep.*
- 16: /cgn2_6/ptodata/2/pubppaa/US10D_PUBCOMB.pep.*
- 17: /cgn2_6/ptodata/2/pubppaa/US10E_PUBCOMB.pep.*
- 18: /cgn2_6/ptodata/2/pubppaa/US10A_NEW_PUB.pep.*
- 19: /cgn2_6/ptodata/2/pubppaa/US11A_PUBCOMB.pep.*
- 20: /cgn2_6/ptodata/2/pubppaa/US11_NEW_PUB.pep.*
- 21: /cgn2_6/ptodata/2/pubppaa/US60_NEW_PUB.pep.*
- 22: /cgn2_6/ptodata/2/pubppaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1558	100.0	1791	10	US-09-983-025-2
2	1303	83.6	1791	9	US-09-827-998-3
3	1303	83.6	1791	15	US-10-675-685-3
4	1299	83.4	1770	9	US-09-827-998-10
5	1299	83.4	1770	15	US-10-675-685-10
6	574	36.8	1385	9	US-09-827-998-16
7	574	36.8	1385	15	US-10-675-685-16
8	192	12.3	192	9	US-09-864-761-34265
9	70	4.5	70	9	US-09-864-761-34264
10	63	4.0	63	9	US-09-864-761-34262
11	18	1.2	704	17	US-10-741-600-1402

12	18	1.2	858	15	US-10-334-143-85	Sequence 85, Appl
13	18	1.2	1232	17	US-10-741-600-1404	Sequence 1404, Ap
14	18	1.2	1420	17	US-10-741-600-1403	Sequence 1403, Ap
15	18	1.2	1420	17	US-10-741-600-1405	Sequence 1405, Ap
16	18	1.2	1547	17	US-10-783-311-2	Sequence 2, Appl1
17	18	1.2	1627	10	US-09-983-025-25	Sequence 25, Appl
18	18	1.2	1627	15	US-10-295-027-663	Sequence 663, App
19	18	1.2	1627	17	US-10-783-311-1	Sequence 1, Appl1
20	18	1.2	1627	17	US-10-741-600-1406	Sequence 1406, Ap
21	18	1.2	1627	17	US-10-991-521-32	Sequence 32, Appl
22	18	1.2	1627	18	US-10-887-229A-8	Sequence 18, Appl
23	11	0.7	20	9	US-09-827-998-18	Sequence 18, Appl
24	11	0.7	20	15	US-10-675-685-18	Sequence 18401, A
25	9	0.6	502	15	US-10-369-493-18401	Sequence 18401, A
26	8	0.5	20	14	US-10-115-072-7	Sequence 7, Appl1
27	8	0.5	20	16	US-10-679-032-45	Sequence 45, Appl
28	8	0.5	28	14	US-10-029-386-30575	Sequence 30575, A
29	8	0.5	43	15	US-10-424-599-243752	Sequence 243752, A
30	8	0.5	66	16	US-10-425-115-352366	Sequence 352366, A
31	8	0.5	87	11	US-09-864-408A-7358	Sequence 7358, Ap
32	8	0.5	117	16	US-10-437-863-137791	Sequence 137791, A
33	8	0.5	118	16	US-10-437-963-129209	Sequence 129209, A
34	8	0.5	145	16	US-10-425-115-301015	Sequence 301015, A
35	8	0.5	153	16	US-10-425-115-301017	Sequence 301017, A
36	8	0.5	158	16	US-10-425-115-358611	Sequence 358611, A
37	8	0.5	173	15	US-10-424-599-211488	Sequence 211488, A
38	8	0.5	194	15	US-10-424-599-261285	Sequence 261285, A
39	8	0.5	202	17	US-10-732-923-15571	Sequence 15571, A
40	8	0.5	204	16	US-10-437-963-195783	Sequence 195783, A
41	8	0.5	221	16	US-10-767-701-32497	Sequence 32497, A
42	8	0.5	274	15	US-10-282-122A-50794	Sequence 50794, A
43	8	0.5	279	15	US-10-424-599-261287	Sequence 261287, A
44	8	0.5	281	15	US-10-282-122A-61115	Sequence 61115, A
45	8	0.5	377	16	US-10-602-898A-14	Sequence 14, Appl

ALIGNMENTS

RESULT 1
US-09-983-025-2
Sequence 2, Application US/09983025
Publication No. US200301245529A1
GENERAL INFORMATION:
APPLICANT: OXVIG, Claus
TITLE OF INVENTION: PREGNANCY-ASSOCIATED PLASMA PROTEIN-A2 (PAP-A2)
FILE REFERENCE: OXVIG-1A
CURRENT APPLICATION NUMBER: US/09/983, 025
CURRENT FILING DATE: 2001-10-22
PRIOR APPLICATION NUMBER: US 60/241, 840
PRIOR FILING DATE: 2000-10-20
PRIOR APPLICATION NUMBER: DK PA 2000 01571
NUMBER OF SEQ ID NOS: 25
SOFTWARE: PatentIn version 3.1
SEQ ID NO 2
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)..(66)
OTHER INFORMATION: prepro part of PAP-A2
NAME/KEY: misc_feature
LOCATION: (67)..(699)
OTHER INFORMATION: pro part of PAP-A2
US-09-983-025-2
Query Match 100.0%; Score 1558; DB 10; Length 1791;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1558; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

QY 1 SPPEESNONGEGSYREAEFTNSQVGLPILYFSGRRERLLRPREVLAETPREAFTVEAMV 60
Db 234 SPPEESNONGEGSYREAEFTNSQVGLPILYFSGRRERLLRPREVLAETPREAFTVEAMV 293
QY 61 KPEGGQNNPAILIAGVFNCSHTVSDKMGALIGSGKDXGKRDARFPFSLCTDRYKATIL 120
Db 294 KPEGGQNNPAILIAGVFNCSHTVSDKMGALIGSGKDXGKRDARFPFSLCTDRYKATIL 353
QY 121 ISHSRYOGTWTVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCSLLLGSSS 180
Db 354 ISHSRYOGTWTVAATYDGRHMALYVDGTQVASSLDQSGPLNSPFMASCSLLLGSSS 413
QY 181 EDGHYFRHGLTGLVFWSTALPOSHFOHSSQHSGBEETDLVLTASFEPVNTWVPRDE 240
Db 414 EDGHYFRHGLTGLVFWSTALPOSHFOHSSQHSGBEETDLVLTASFEPVNTWVPRDE 473
QY 241 KYPRLEVLQGFPEPEBELISPLQPPICGQTVCDNVELISQYNGWPLRGEKVIROYVNIC 300
Db 474 KYPRLEVLQGFPEPEBELISPLQPPICGQTVCDNVELISQYNGWPLRGEKVIROYVNIC 533
QY 301 DDEGLNPVSEEOJRLQHEALNEAFSRYNISMOZSVHGVNSTLRHRVVLVNCBPSKIGN 360
Db 534 DDEGLNPVSEEOJRLQHEALNEAFSRYNISMOZSVHGVNSTLRHRVVLVNCBPSKIGN 593
QY 361 DHCDPECEHPLTGYDGDGDLQGRCYSWNRBDGLCHVCNNMLNDFDGDCCDQVADVR 420
Db 594 DHCDPECEHPLTGYDGDGDLQGRCYSWNRBDGLCHVCNNMLNDFDGDCCDQVADVR 653
QY 421 KTCEDPDSPKRAYSVKELKALQNLSTHPLNTYFASVREDLAGAATWPMKDCAVTHLG 480
Db 654 KTCEDPDSPKRAYSVKELKALQNLSTHPLNTYFASVREDLAGAATWPMKDCAVTHLG 713
QY 481 GIVLSPAYYGMRGHTDPMIHEGVHVLGLYHVFKEYVSEESGNDCKEVPMEETGDLCAD 540
Db 714 GIVLSPAYYGMRGHTDPMIHEGVHVLGLYHVFKEYVSEESGNDCKEVPMEETGDLCAD 773
QY 541 TAPTPKSELCREPEPTSDTCGFTTRPGAFPTNYMSYTDNCTDNFTPNQVARMHCYLDLV 600
Db 774 TAPTPKSELCREPEPTSDTCGFTTRPGAFPTNYMSYTDNCTDNFTPNQVARMHCYLDLV 833
QY 601 YQOMTESAKPPIPIPPMVIQOTNKSLLTIHMLPPISGVYVYRASGSLCGACTEBGTROY 660
Db 834 YQOMTESAKPPIPIPPMVIQOTNKSLLTIHMLPPISGVYVYRASGSLCGACTEBGTROY 893
QY 661 VHTSSRRVCSGSGWPEBAVGPDDVQPCBPSLOQASPEVHL YHMMWTPCPTBEGSL 720
Db 894 VHTSSRRVCSGSGWPEBAVGPDDVQPCBPSLOQASPEVHL YHMMWTPCPTBEGSL 953
QY 721 ELRFQHPVQADTLTLMTVSFPMESSQVLFDEIILENKESVHLGPLDTFCDIPLTIKLHV 780
Db 954 ELRFQHPVQADTLTLMTVSFPMESSQVLFDEIILENKESVHLGPLDTFCDIPLTIKLHV 1013
QY 781 DGKVSQVYVTFDERIEIDALLTSQPHSPLCSGCRPRYVULRDPFASGLPVVVTHSH 840
Db 1014 DGKVSQVYVTFDERIEIDALLTSQPHSPLCSGCRPRYVULRDPFASGLPVVVTHSH 1073
QY 841 RKFTDVEVTPEOMYOYVLAAGELGASPLNHHINGAPVCGSGKXSERLGEBCDDGL 900
Db 1074 RKFTDVEVTPEOMYOYVLAAGELGASPLNHHINGAPVCGSGKXSERLGEBCDDGL 1133
QY 901 VSGDGSQVCELEBGFNCVGBPSLCYMYEGDGI CEPEFRKTSIYDCGITYPKGYLDQMAT 960
Db 1134 VSGDGSQVCELEBGFNCVGBPSLCYMYEGDGI CEPEFRKTSIYDCGITYPKGYLDQMAT 1193
QY 961 RAYSHEHDKKCYVSLVTGBPHSLICTSYHPDLPNHRPLTWMPQCVASENETQDRSEOP 1020
Db 1194 RAYSHEHDKKCYVSLVTGBPHSLICTSYHPDLPNHRPLTWMPQCVASENETQDRSEOP 1253
QY 1021 BGSJLKKDEWMLKXCFNRPGBARAIFLTLTDGLVPGHOOPUTVITYLVDRSGNHSISGT 1080
Db 1254 BGSJLKKDEWMLKXCFNRPGBARAIFLTLTDGLVPGHOOPUTVITYLVDRSGNHSISGT 1313
QY 1081 YGLSCQHNPLIINVTTHQNVLFHHTTSVTLNFSSPRVGISAVALRTSRIGLSAPNSCIS 1140

```

```

Db 1314 YGLSCQHNPLIINVTTHQNVLFHHTTSVTLNFSSPRVGISAVALRTSRIGLSAPNSCIS 1373
QY 1141 EDEGQNHQGSCTHRPGCKDSCPSILLDHDVNVNCTISIBGLMKCAITQORGALQASS 1200
Db 1374 EDEGQNHQGSCTHRPGCKDSCPSILLDHDVNVNCTISIBGLMKCAITQORGALQASS 1433
QY 1201 GQYIRPMQKEILLTCSGSHMDQNVSCLPVDCGVDPDPBLVNVANFSCSEGTFLKRCISISC 1260
Db 1434 GQYIRPMQKEILLTCSGSHMDQNVSCLPVDCGVDPDPBLVNVANFSCSEGTFLKRCISISC 1493
QY 1261 VPPAKLOGLSPWLTCLLEDGLMSLPREVYCKLECDAPPIILNANILLPHCLQDNHVGITIC 1320
Db 1494 VPPAKLOGLSPWLTCLLEDGLMSLPREVYCKLECDAPPIILNANILLPHCLQDNHVGITIC 1553
QY 1321 YECKRGTYYVAESAEGKRNLLKTIQCLEGGIWEQSGCIPVCEPPRPVFGMTGECTGFS 1380
Db 1554 YECKRGTYYVAESAEGKRNLLKTIQCLEGGIWEQSGCIPVCEPPRPVFGMTGECTGFS 1613
QY 1381 LDSQCVLNCQBERKPLILCTKEGLMTQEFKLCENIQEGCPPRPSBLNSVEYKCEQYGI 1440
Db 1614 LDSQCVLNCQBERKPLILCTKEGLMTQEFKLCENIQEGCPPRPSBLNSVEYKCEQYGI 1673
QY 1441 GAVCSPLCVIIPSPDPVNL PENITADTL EHMMEPVKVOSIYCTGRQNHDPVLVHCIOQC 1500
Db 1674 GAVCSPLCVIIPSPDPVNL PENITADTL EHMMEPVKVOSIYCTGRQNHDPVLVHCIOQC 1733
QY 1501 EPPQADGMDCTINNRAACHVDGDCSSSTLSKKVLPFADCDLDECTCRDPKAEENO 1558
Db 1734 EPPQADGMDCTINNRAACHVDGDCSSSTLSKKVLPFADCDLDECTCRDPKAEENO 1791

RESULT 2
US-09-827-998-3
; Sequence 3, Application US/09827998
; Patent No. US20020102252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mack
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMPF-8
; CURRENT APPLICATION NUMBER: US/09/827, 998
; PRIOR FILING DATE: 2001-04-06
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/207, 456
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 3
; LENGTH: 1791
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-3

Query Match 83.6%; Score 1303; DB 9; Length 1791;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1503; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

414 EDGHYFRGHJLCTVFMWSTALPQSHFQSSQHSSEEBATDVLVLASFEFVNTWMPFRDE 473
QY 241 KYRPLEVLQGFEBEPBELLSPLOPPLCGQTVCDNVELISQNGYVPLBGEKIRYQVNIC 300
Db 474 KYRPLEVLQGFEBEPBELLSPLOPPLCGQTVCDNVELISQNGYVPLBGEKIRYQVNIC 533
QY 301 DDEGLNPVSEBQIRLQHEALNEAFSRYNISWQLSVQVHNSTLRHRVVLVNCPSKIGN 360
Db 534 DDEGLNPVSEBQIRLQHEALNEAFSRYNISWQLSVQVHNSTLRHRVVLVNCPSKIGN 593
QY 361 DHCPECEHPLTGYDGDGDLQGRCYSWNRDGLCHVECNMMLNDFDGDCCDQVADVR 420
Db 594 DHCPECEHPLTGYDGDGDLQGRCYSWNRDGLCHVECNMMLNDFDGDCCDQVADVR 653
QY 421 KTCEDPSPKRAYSVKELKALQLNSTHPLNTYFASVREDLGAATWPDKXAVTHLG 480
Db 654 KTCEDPSPKRAYSVKELKALQLNSTHPLNTYFASVREDLGAATWPDKXAVTHLG 713
QY 481 GIVLSPAYYGMFGHTDMHVEGHVGLYHVFQGVSEBESGNDCKETVSPMETGDLCAD 540
Db 714 GIVLSPAYYGMFGHTDMHVEGHVGLYHVFQGVSEBESGNDCKETVSPMETGDLCAD 773
QY 541 TAPPKSELCREPPTSOTCGFTRPGAFTNYSYTDNCTDNFTPNQVARMHCYLDLV 600
Db 774 TAPPKSELCREPPTSOTCGFTRPGAFTNYSYTDNCTDNFTPNQVARMHCYLDLV 833
QY 601 YQOMTESRKPTPIPIPMVIGQTNKSLTIHMLPRISGVYVDRASGSLCGACTEDGTRQY 660
Db 834 YQOMTESRKPTPIPIPMVIGQTNKSLTIHMLPRISGVYVDRASGSLCGACTEDGTRQY 893
QY 661 VHTSSRRVCDSSGVTMBEAVGPVDQCEPSLOASPEVHLVHMNMVPCTEGSL 720
Db 894 VHTSSRRVCDSSGVTMBEAVGPVDQCEPSLOASPEVHLVHMNMVPCTEGSL 953
QY 721 ELTFQHFVQADTLTLMWTSFFMSSQVLFDEIILLENKESYHGLPLDFCDIPITIKLHV 780
Db 954 ELTFQHFVQADTLTLMWTSFFMSSQVLFDEIILLENKESYHGLPLDFCDIPITIKLHV 1013
QY 781 DGKVSQVYVTFDERIEIDALLTSQHSPLCSGCRPVRYVTLRDPFASGLPVVYTHSH 840
Db 1014 DGKVSQVYVTFDERIEIDALLTSQHSPLCSGCRPVRYVTLRDPFASGLPVVYTHSH 1073
QY 841 RKFTDVVTGQMYOYVLAAGELGASPLNHNHIGAPVCGQKXSERLGECCDGD 900
Db 1074 RKFTDVVTGQMYOYVLAAGELGASPLNHNHIGAPVCGQKXSERLGECCDGD 1133
QY 901 VSGDGCSCVCELEEGFNCVCEPSLCYMYEGDICEPERKTSIVDCGIYTPKGYLDQWAT 960
Db 1134 VSGDGCSCVCELEEGFNCVCEPSLCYMYEGDICEPERKTSIVDCGIYTPKGYLDQWAT 1193
QY 961 RAYSHEDKKKCPVSLVTGBEBSLICTSYHBDLPNHRPLTGMPPCVASENETODRSEBP 1020
Db 1194 RAYSHEDKKKCPVSLVTGBEBSLICTSYHBDLPNHRPLTGMPPCVASENETODRSEBP 1253
QY 1021 EGSJAKKEDVWLKCFNRPGARAIFFLTDTGVPGEHQPTVTLVLTIVRGSNHSIGT 1080
Db 1254 EGSJAKKEDVWLKCFNRPGARAIFFLTDTGVPGEHQPTVTLVLTIVRGSNHSIGT 1313
QY 1081 YGSLSCQNPPLINTVTHQNVLFHHTTSVLFNFSFPRVIGISAVALRTSSRIGLSAPNSCIS 1140
Db 1314 YGSLSCQNPPLINTVTHQNVLFHHTTSVLFNFSFPRVIGISAVALRTSSRIGLSAPNSCIS 1373
QY 1141 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNTCSIGBLMKCAITTCRGFALQASS 1200
Db 1374 EDEGQNHQGSCHIRPCGKODSCPSLLLDHADVNTCSIGBLMKCAITTCRGFALQASS 1433
QY 1201 GOVYRPMOKETILLTCSGSHMDQVNSCLPVOCGPVDPSPVNYANFSCBEGTFLRCSISIC 1260
Db 1434 GOVYRPMOKETILLTCSGSHMDQVNSCLPVOCGPVDPSPVNYANFSCBEGTFLRCSISIC 1493
QY 1261 VPPAKLOGLSFWLCTLEDGLMSLPEVYCKLECDAPPIILNANLPLPCLQDNHVDGTCIK 1320
Db 1494 VPPAKLOGLSFWLCTLEDGLMSLPEVYCKLECDAPPIILNANLPLPCLQDNHVDGTCIK 1553

QY 1321 YECKPGYVAESAGKVRNKLKTIQCEGGIWEQSGCIPVCEBPPPVFEGMVECTNGFS 1380
Db 1554 YECKPGYVAESAGKVRNKLKTIQCEGGIWEQSGCIPVCEBPPPVFEGMVECTNGFS 1613
QY 1381 LDSQCVLNCQERREKLILCTKEGLMTQEFPLCENLQGECPPPSELSNVEYKCEQYGI 1440
Db 1614 LDSQCVLNCQERREKLILCTKEGLMTQEFPLCENLQGECPPPSELSNVEYKCEQYGI 1673
QY 1441 GAVCSPLCVIPSPDPMVLPENTVADTLEHNMPEYKVOSIVCTGRQWHPDVLVHCIOQC 1500
Db 1674 GAVCSPLCVIPSPDPMVLPENTVADTLEHNMPEYKVOSIVCTGRQWHPDVLVHCIOQC 1733
QY 1501 EPPQA 1505
Db 1734 EPPQA 1738

RESULT 3
US-10-675-685-3
Sequence 3, Application US/10675685
Publication No. US20040063134A1
GENERAL INFORMATION:
APPLICANT: Gu, Yizhong
APPLICANT: Shannon, Mark
TITLE OR INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
FILE REFERENCE: PB0114
CURRENT APPLICATION NUMBER: US/10/675, 685
PRIOR FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Aeomica Sequence Listing Engine
SEQ ID NO 3
LENGTH: 1791
TYPE: PRT
ORGANISM: Homo sapiens
US-10-675-685-3

Query Match 83.6%; Score 1303; DB 15; Length 1791;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1503; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY 1 SPRESNONGEGSYREAEFTNSQVGLPIYFSGRRRLLRPEVLAIPREAEFTVEAMV 60
Db 234 SPRESNONGEGSYREAEFTNSQVGLPIYFSGRRRLLRPEVLAIPREAEFTVEAMV 293
QY 61 KPREGQNNPAILIAGVFNCSHTTSDKGMALGIRGKXKGRDAPFPFSLCTDRYKXATIL 120
Db 294 KPREGQNNPAILIAGVFNCSHTTSDKGMALGIRGKXKGRDAPFPFSLCTDRYKXATIL 353
QY 121 ISHSRYQPGTWTHAAYTDGRHMLVYDGTQVNASLDSQGPLNSPPMASCSRLLGDS 180
Db 354 ISHSRYQPGTWTHAAYTDGRHMLVYDGTQVNASLDSQGPLNSPPMASCSRLLGDS 413
QY 181 EDGHYFRGHJLCTVFMWSTALPQSHFQSSQHSSEEBATDVLVLASFEFVNTWMPFRDE 240
Db 414 EDGHYFRGHJLCTVFMWSTALPQSHFQSSQHSSEEBATDVLVLASFEFVNTWMPFRDE 473
QY 241 KYRPLEVLQGFEBEPBELLSPLOPPLCGQTVCDNVELISQNGYVPLBGEKIRYQVNIC 300
Db 474 KYRPLEVLQGFEBEPBELLSPLOPPLCGQTVCDNVELISQNGYVPLBGEKIRYQVNIC 533
QY 301 DDEGLNPVSEBQIRLQHEALNEAFSRYNISWQLSVQVHNSTLRHRVVLVNCPSKIGN 360
Db 534 DDEGLNPVSEBQIRLQHEALNEAFSRYNISWQLSVQVHNSTLRHRVVLVNCPSKIGN 593
QY 361 DHCPECEHPLTGYDGDGDLQGRCYSWNRDGLCHVECNMMLNDFDGDCCDQVADVR 420
Db 594 DHCPECEHPLTGYDGDGDLQGRCYSWNRDGLCHVECNMMLNDFDGDCCDQVADVR 653

```

QY 421 KTCFDPSPKRAYMSVKEALKEALQLNSTHPLNIFYFASVREDLAGAATWMDKDAVTHLG 480
DB 654 KTCFDPSPKRAYMSVKEALKEALQLNSTHPLNIFYFASVREDLAGAATWMDKDAVTHLG 713
QY 481 GIVLSPAYVGMPGHTDMIHVEGVHVLGLYHVFKGVSERESCNDRCKETVPSMETGDLCAD 540
DB 714 GIVLSPAYVGMPGHTDMIHVEGVHVLGLYHVFKGVSERESCNDRCKETVPSMETGDLCAD 773
QY 541 TAPTPKSELCREPEPTSDTCGFTFRPGAPFTNWSYTDNDCTDNFTNOVABMHICYDLV 600
DB 774 TAPTPKSELCREPEPTSDTCGFTFRPGAPFTNWSYTDNDCTDNFTNOVABMHICYDLV 833
QY 601 YQOWTESRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEDGTEROY 660
DB 834 YQOWTESRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEDGTEROY 893
QY 661 VHTASSRRVCDSSGYWTPPEAVGPPDVDOCPCEPSLOAMSPEVHLYHMMVTPCETEGCSL 720
DB 894 VHTASSRRVCDSSGYWTPPEAVGPPDVDOCPCEPSLOAMSPEVHLYHMMVTPCETEGCSL 953
QY 721 ELFLFOHVOADTLTLMTSPFMSSOVLFDTEILLNKESVHGLPLDTCODIPLTLIKLV 780
DB 954 ELFLFOHVOADTLTLMTSPFMSSOVLFDTEILLNKESVHGLPLDTCODIPLTLIKLV 1013
QY 781 DGKTVGKVTYFDBRIEIDALLTSOPHSPLCSGCRPYRYOVLADPPASGLPVVYTHSH 840
DB 1014 DGKTVGKVTYFDBRIEIDALLTSOPHSPLCSGCRPYRYOVLADPPASGLPVVYTHSH 1073
QY 841 RKFTDVEVTPGOMYOYOVLABAGELGASPLNHIHIGAPYCGDGKXSERLGEBCDDGL 900
DB 1074 RKFTDVEVTPGOMYOYOVLABAGELGASPLNHIHIGAPYCGDGKXSERLGEBCDDGL 1133
QY 901 VSGGSCKVCLEBEGFNCVGPBSLCYMEGDCICEPERKTSYVDCGITYPKGLDQWAT 960
DB 1134 VSGGSCKVCLEBEGFNCVGPBSLCYMEGDCICEPERKTSYVDCGITYPKGLDQWAT 1193
QY 961 RAYSHSHDKKCPVSLVTGEBSHSLICTSYHBDLPNHRPLTGMFPCVASENETQDRSEOP 1020
DB 1194 RAYSHSHDKKCPVSLVTGEBSHSLICTSYHBDLPNHRPLTGMFPCVASENETQDRSEOP 1253
QY 1021 EGSIKKEDVWLKVCENRPGBARAIFLFTLTDGLVGEHQPTVTLVLTVDVRSNHSLSGT 1080
DB 1254 EGSIKKEDVWLKVCENRPGBARAIFLFTLTDGLVGEHQPTVTLVLTVDVRSNHSLSGT 1313
QY 1081 YGSLSCOHNPRLINTYHONVLFHHTTSVLTNPSRPGISAVARTSRIGLSAPNSCTIS 1140
DB 1314 YGSLSCOHNPRLINTYHONVLFHHTTSVLTNPSRPGISAVARTSRIGLSAPNSCTIS 1373
QY 1141 EDEGONHOGOSCIHRPCGKODSCPSLLDHDVNNCTSIGGLMKCAITTCORGFALQASS 1200
DB 1374 EDEGONHOGOSCIHRPCGKODSCPSLLDHDVNNCTSIGGLMKCAITTCORGFALQASS 1433
QY 1201 GOYIRPMQKELITLTCSSGHWQDNVSLPVDGVPDPSSLVNYANFSCSEBGTFLKRCISISC 1260
DB 1434 GOYIRPMQKELITLTCSSGHWQDNVSLPVDGVPDPSSLVNYANFSCSEBGTFLKRCISISC 1493
QY 1261 VPPAKLOGSLFWLTCLEBDGLMSLPEVYCKLECDAPRIILNANLILPHLODNHNVGTITCK 1320
DB 1494 VPPAKLOGSLFWLTCLEBDGLMSLPEVYCKLECDAPRIILNANLILPHLODNHNVGTITCK 1553
QY 1321 YECRPGYVVASASGKVNKLKLTQCLEGGIWEOSCIPIVCEPPRPVFEGBMEYCTNGFS 1380
DB 1554 YECRPGYVVASASGKVNKLKLTQCLEGGIWEOSCIPIVCEPPRPVFEGBMEYCTNGFS 1613
QY 1381 LDSQCVLNCNOREKRLPLCTKEGLWTOEFYLCENLQCECPPPSESLNSVAYKCEOGYGI 1440
DB 1614 LDSQCVLNCNOREKRLPLCTKEGLWTOEFYLCENLQCECPPPSESLNSVAYKCEOGYGI 1673
QY 1441 GAVVSPCLCVIPSPDVMLENITADTLEHMMEPKVOSIVCTGRGOWHPPDVVHNCIOSC 1500
DB 1674 GAVVSPCLCVIPSPDVMLENITADTLEHMMEPKVOSIVCTGRGOWHPPDVVHNCIOSC 1733
QY 1501 EPPQA 1505

```

```

DB 1734 EPPQA 1738

RESULT 4
US-09-827-998-10
; Sequence 10, Application US/09827998
; Patent No. US2002010252A1
; GENERAL INFORMATION:
; APPLICANT: Gu, Yizhong
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E
; FILE REFERENCE: MDHMOF-8
; CURRENT FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 10
; LENGTH: 1770
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-10

```

Query Match 83.4%; Score 1299; DB 9; Length 1770;

Best Local Similarity 99.9%; Pred. No. 0; Matches 1499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

```

QY 1 SPPESSNONGGEGSYREARETFNSQVGLPIYFSGRRRLLRPEVLAIEPREAFTVEAWY 60
DB 234 SPPESSNONGGEGSYREARETFNSQVGLPIYFSGRRRLLRPEVLAIEPREAFTVEAWY 293
QY 61 KPEGQNNPAILAGVPDNCSTHTVSDKGWALGIRSGKDKGRDARFFPSLCTDRYKATIL 120
DB 294 KPEGQNNPAILAGVPDNCSTHTVSDKGWALGIRSGKDKGRDARFFPSLCTDRYKATIL 353
QY 121 ISHSRYQPGTWTVAAYTDDRHMAALVYDGTQVASSLDQSPPLNSPFMASSCRSLILGSDS 180
DB 354 ISHSRYQPGTWTVAAYTDDRHMAALVYDGTQVASSLDQSPPLNSPFMASSCRSLILGSDS 413
QY 181 EDGHYFRGHGLGTIVFMSTALPQSHFOHSSQHSSEBEATDLVLASFEVNTENWVPRDE 240
DB 414 EDGHYFRGHGLGTIVFMSTALPQSHFOHSSQHSSEBEATDLVLASFEVNTENWVPRDE 473
QY 241 KYPLREVLQGFPEPEPILSPLOPPLCGQIVCDNVELISQYNGTWPLRGEKVIROYVNIC 300
DB 474 KYPLREVLQGFPEPEPILSPLOPPLCGQIVCDNVELISQYNGTWPLRGEKVIROYVNIC 533
QY 301 DDEGLNIVSEBOIRLOHEALNFAFSRYNISWOLSVHQNSTLRHVVLVNCPSKIGN 360
DB 534 DDEGLNIVSEBOIRLOHEALNFAFSRYNISWOLSVHQNSTLRHVVLVNCPSKIGN 593
QY 361 DHCDPECEHPLTGDGDCRLQGRCYSMNRDGLCHVECNMNLDPDGDCCDPQVADV 420
DB 594 DHCDPECEHPLTGDGDCRLQGRCYSMNRDGLCHVECNMNLDPDGDCCDPQVADV 653
QY 421 KTCFDPSPKRAYMSVKEALKEALQLNSTHPLNIFYFASVREDLAGAATWMDKDAVTHLG 480
DB 654 KTCFDPSPKRAYMSVKEALKEALQLNSTHPLNIFYFASVREDLAGAATWMDKDAVTHLG 713
QY 481 GIVLSPAYVGMPGHTDMIHVEGVHVLGLYHVFKGVSERESCNDRCKETVPSMETGDLCAD 540
DB 714 GIVLSPAYVGMPGHTDMIHVEGVHVLGLYHVFKGVSERESCNDRCKETVPSMETGDLCAD 773
QY 541 TAPTPKSELCREPEPTSDTCGFTFRPGAPFTNWSYTDNDCTDNFTNOVABMHICYDLV 600
DB 774 TAPTPKSELCREPEPTSDTCGFTFRPGAPFTNWSYTDNDCTDNFTNOVABMHICYDLV 833
QY 601 YQOWTESRKPTPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLCGACTEDGTEROY 660

```

834 YQWWTESRKPPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLGACTEDTFRQY 893
661 VHTASRRVCDSSGYWTPBEAVGPPDVQPCBPSTQAMSPVHLVHMNTVPCPREGSL 720
894 VHTASRRVCDSSGYWTPBEAVGPPDVQPCBPSTQAMSPVHLVHMNTVPCPREGSL 953
721 ELTFQHPVQADTLTLMTWTSFPMESQVLPTEILLENKESVHLGDLTFCDIPLTIKLV 780
954 ELTFQHPVQADTLTLMTWTSFPMESQVLPTEILLENKESVHLGDLTFCDIPLTIKLV 1013
781 DGKVSQVKTVPFDERIEIDALLTSQPHSLCSGCRPVRYQVLRDPFASGLPVVVTSH 840
1014 DGKVSQVKTVPFDERIEIDALLTSQPHSLCSGCRPVRYQVLRDPFASGLPVVVTSH 1073
841 RKFPDVEVTGROMVOYVLAAGGELGRASPPMTHIHAPVCGDGKVSERLGEEDDDGL 900
1074 RKFPDVEVTGROMVOYVLAAGGELGRASPPMTHIHAPVCGDGKVSERLGEEDDDGL 1133
901 VSGDGSQVCELEBGFNCVGPSPSLCYMEGDOI CEFPFRKTSYVDCGIYTPKGYLDOMAT 960
1134 VSGDGSQVCELEBGFNCVGPSPSLCYMEGDOI CEFPFRKTSYVDCGIYTPKGYLDOMAT 1193
961 RAYSSHEDKKKCPVSLVTGEPHSLICTSYHPLDPMHRLTGMFPCVASENETODDRSOP 1020
1194 RAYSSHEDKKKCPVSLVTGEPHSLICTSYHPLDPMHRLTGMFPCVASENETODDRSOP 1253
1021 BGLSLKEDBEVWLKVCENRPGEARAIFITLTDGLVGHQOFTVTLTYTDVRSNHSIGT 1080
1254 BGLSLKEDBEVWLKVCENRPGEARAIFITLTDGLVGHQOFTVTLTYTDVRSNHSIGT 1313
1081 YGLSCOHNPLIINTYHONVLFHHTTSVLTNPSRPGISAVALTSSRIGLSAPNSCTIS 1140
1314 YGLSCOHNPLIINTYHONVLFHHTTSVLTNPSRPGISAVALTSSRIGLSAPNSCTIS 1373
1141 EDEGQNHQGSQVSIHRPCGKODSCPSLLDHDVNVCTSIGPLMKCAITTCORGFALQSS 1200
1374 EDEGQNHQGSQVSIHRPCGKODSCPSLLDHDVNVCTSIGPLMKCAITTCORGFALQSS 1433
1201 GQYIRPMQKELLTCSSGHWQONVSLPVDGVPDPSSLVNYANFSCSEGTPLKRCSTISC 1260
1434 GQYIRPMQKELLTCSSGHWQONVSLPVDGVPDPSSLVNYANFSCSEGTPLKRCSTISC 1493
1261 VPRAKLGLSPMLTCLBEGMLSLPEVYKCLBDAPIITLNNALLPHCLQNHVGTCTCK 1320
1494 VPRAKLGLSPMLTCLBEGMLSLPEVYKCLBDAPIITLNNALLPHCLQNHVGTCTCK 1553
1321 YECKRQYVVASASGKRNKLLKIQCLEGGIMEQSCIPVCEPPRPVFEQMECTNGFS 1380
1554 YECKRQYVVASASGKRNKLLKIQCLEGGIMEQSCIPVCEPPRPVFEQMECTNGFS 1613
1381 LDSQCVLNCQERELPLCTKEGIMTQEFKLCENLQCECPRPSELSNVEYKCEQGYGI 1440
1614 LDSQCVLNCQERELPLCTKEGIMTQEFKLCENLQCECPRPSELSNVEYKCEQGYGI 1673
1441 GAVSPLCVIPSPDPMLENTADTLEHMMEPKVQSVICTGRQWHPDVLVHCTOSC 1500
1674 GAVSPLCVIPSPDPMLENTADTLEHMMEPKVQSVICTGRQWHPDVLVHCTOSC 1733
1501 E 1501
1734 E 1734

RESULT 5
US-10-675-685-10

; Sequence 10, Application US/10675685
; Publication No. US2004006313441

; GENERAL INFORMATION:

; APPLICANT: Gu, Yizhong

; APPLICANT: Shannon, Mark

; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

; FILE REFERENCE: PB0114

; CURRENT APPLICATION NUMBER: US/10/675,685

CURRENT FILING DATE: 2003-09-30
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
PRIOR APPLICATION NUMBER: US 60/236,359
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 1881
SOFTWARE: Acomica Sequence Listing Engine
SEQ ID NO 10
LENGTH: 1770
TYPE: PRT
ORGANISM: Homo sapiens
US-10-675-685-10

Query Match 83.4%; Score 1299; DB 15; Length 1770;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 1499; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

1 SPPESSNONGEGSYREARETFNSQVGLPIYFSGRRELLRPREVLAETPREAFTVEMV 60
234 SPPESSNONGEGSYREARETFNSQVGLPIYFSGRRELLRPREVLAETPREAFTVEMV 293
61 KPEGQNNPALLIAGVFNCSHTVSDKGWALGIRSGKDKRDAFFPSGLCTDRVKKATIL 120
294 KPEGQNNPALLIAGVFNCSHTVSDKGWALGIRSGKDKRDAFFPSGLCTDRVKKATIL 353
121 ISHSRYQGTWTHAATYDGHMALLYDGTQVASSLDQSGFLNPFMASSCSLLIGDSS 180
354 ISHSRYQGTWTHAATYDGHMALLYDGTQVASSLDQSGFLNPFMASSCSLLIGDSS 413
181 EDGHPFGHGLTGLFWSHTALPQSHFQSSQSSGSEBEATDLVLTASFPEVNTWMPFDE 240
414 EDGHPFGHGLTGLFWSHTALPQSHFQSSQSSGSEBEATDLVLTASFPEVNTWMPFDE 473
241 KYRPLEVLQGFEPPEILSLQPPVLCQTVQCNVELISQYNGWPLRGEKVIYQVNVIC 300
474 KYRPLEVLQGFEPPEILSLQPPVLCQTVQCNVELISQYNGWPLRGEKVIYQVNVIC 533
301 DDEGLNPVSEBQRLQHEALNEAFSRYNISWQLSVHOVNSTLRHRYVLYNCEBSKIGN 360
534 DDEGLNPVSEBQRLQHEALNEAFSRYNISWQLSVHOVNSTLRHRYVLYNCEBSKIGN 593
361 DHCPBECHPLTGYDGDGCRLOGRCYSMNRDGLCHVECNMMLNDPDDGDCDDQVAVR 420
594 DHCPBECHPLTGYDGDGCRLOGRCYSMNRDGLCHVECNMMLNDPDDGDCDDQVAVR 653
421 KTCFDPSPKRAYSVKELKALQNLNSTHPLNIYFASVREDLAAGATWPKDXAVTHLG 480
654 KTCFDPSPKRAYSVKELKALQNLNSTHPLNIYFASVREDLAAGATWPKDXAVTHLG 713
481 GIVLSPAYYGMPGHTMTIHEVGHVGLYHVKQVSERESGNDPCKETVPSMETGDLCAD 540
714 GIVLSPAYYGMPGHTMTIHEVGHVGLYHVKQVSERESGNDPCKETVPSMETGDLCAD 773
541 TAPPKSELCREPPTSDTQGFTRPGAPFNWVSYYDNDCTDFTPQVARMKCYLDLV 600
774 TAPPKSELCREPPTSDTQGFTRPGAPFNWVSYYDNDCTDFTPQVARMKCYLDLV 833
601 YQWWTESRKPPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLGACTEDTFRQY 660
834 YQWWTESRKPPIPIPMVIGQTNKSLTIHMLPISGVVYDRASGSLGACTEDTFRQY 893
661 VHTASRRVCDSSGYWTPBEAVGPPDVQPCBPSTQAMSPVHLVHMNTVPCPREGSL 720
894 VHTASRRVCDSSGYWTPBEAVGPPDVQPCBPSTQAMSPVHLVHMNTVPCPREGSL 953
721 ELTFQHPVQADTLTLMTWTSFPMESQVLPTEILLENKESVHLGDLTFCDIPLTIKLV 780
954 ELTFQHPVQADTLTLMTWTSFPMESQVLPTEILLENKESVHLGDLTFCDIPLTIKLV 1013
781 DGKVSQVKTVPFDERIEIDALLTSQPHSLCSGCRPVRYQVLRDPFASGLPVVVTSH 840
1014 DGKVSQVKTVPFDERIEIDALLTSQPHSLCSGCRPVRYQVLRDPFASGLPVVVTSH 1073

Qy 841 RKFTDVEVTGQMYQYVLAAGGELGSEASPLNHIHGA PYCGDKYSERLGECCDDGL 900
Db 1074 RKFTDVEVTGQMYQYVLAAGGELGSEASPLNHIHGA PYCGDKYSERLGECCDDGL 1133
Qy 901 VSGDGSKYCELEBGFNCVGEPSLCYMEGDGICEPFRKTSIYDCGIYTPKGYLDQWAT 960
Db 1134 VSGDGSKYCELEBGFNCVGEPSLCYMEGDGICEPFRKTSIYDCGIYTPKGYLDQWAT 1193
Qy 961 RAYSHHEKXKCPVSLVYGEBSHLSICTSYHPDLPHNRPLTGMPCVASENTOODRSQOP 1020
Db 1194 RAYSHHEKXKCPVSLVYGEBSHLSICTSYHPDLPHNRPLTGMPCVASENTOODRSQOP 1253
Qy 1021 EGSJKEDEBVMKVCENRPGEARAIFILTTDGLVGEHQOPTYTLVLTVDVRSNHSIGT 1080
Db 1254 EGSJKEDEBVMKVCENRPGEARAIFILTTDGLVGEHQOPTYTLVLTVDVRSNHSIGT 1313
Qy 1081 YGLSCQHNPLIINTVTHQNVLFHHTTSYLVNFPSSPRVGISAVALTSSRIGLSAPNSCIS 1140
Db 1314 YGLSCQHNPLIINTVTHQNVLFHHTTSYLVNFPSSPRVGISAVALTSSRIGLSAPNSCIS 1373
Qy 1141 EDEGQNHQGSCHIRPCGKQDCPSLLLDHADVNCISIGPLMKCAITTCQGFALQAS 1200
Db 1374 EDEGQNHQGSCHIRPCGKQDCPSLLLDHADVNCISIGPLMKCAITTCQGFALQAS 1433
Qy 1201 GQYIRPMQKEIILTCSSGHDQNVSCLPVDCGVPDPSLVNYANFSCSEBGTFLKRCISIC 1260
Db 1434 GQYIRPMQKEIILTCSSGHDQNVSCLPVDCGVPDPSLVNYANFSCSEBGTFLKRCISIC 1493
Qy 1261 VPPAKLQGLSPWLTCLLEDGLMSLPEVYCKLECDAPPIILNANLLPHCLQDNHVDGTTCK 1320
Db 1494 VPPAKLQGLSPWLTCLLEDGLMSLPEVYCKLECDAPPIILNANLLPHCLQDNHVDGTTCK 1553
Qy 1321 YECPRGYVAASABSKVANKLKIQCLEGGIMEGSSCIPVCEPPRPVEBAMECTGNS 1380
Db 1554 YECPRGYVAASABSKVANKLKIQCLEGGIMEGSSCIPVCEPPRPVEBAMECTGNS 1613
Qy 1381 LDSQCVLNCQREKLPILCTKEGLMTQEFKLCENLQGECPRPPELSNVEYKCEQGYGI 1440
Db 1614 LDSQCVLNCQREKLPILCTKEGLMTQEFKLCENLQGECPRPPELSNVEYKCEQGYGI 1673
Qy 1441 GAVCSPLCVIIPSPDPMLENITADTLEHMEPVKVQSIYCTGRQWHPDVLVHCIOQC 1500
Db 1674 GAVCSPLCVIIPSPDPMLENITADTLEHMEPVKVQSIYCTGRQWHPDVLVHCIOQC 1733
Qy 1501 E 1501
Db 1734 E 1734

RESULT 6
US-09-827-998-16
; Sequence 16, Application US/09827998
; Patent No. US2002010252A1
; GENERAL INFORMATION:
; APPLICANT: Shannon, Mark
; TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN B
; FILE REFERENCE: MDIMORF-8
; CURRENT APPLICATION NUMBER: US/09/827,998
; PRIOR FILING DATE: 2001-04-06
; PRIOR APPLICATION NUMBER: US 60/207,456
; PRIOR FILING DATE: 2000-05-26
; PRIOR APPLICATION NUMBER: US 60/236,359
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 1881
; SOFTWARE: Aecomica Sequence Listing Engine
; SEQ ID NO 16
; LENGTH: 1385
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-827-998-16

Query Match 36.8%; Score 574; DB 9; Length 1385;

Best Local Similarity 99.5%; Pred. No. 0;
Matches 1074; Conservative 0; Mismatches 5; Indels 0; Gaps 0;
Qy 480 GGIVLSAAYYGMGDHDTMHEVGHVLYGLVHFVGVSERSCNDCPKETVPSMETGLCA 539
Db 307 GGIVLSAAYYGMGDHDTMHEVGHVLYGLVHFVGVSERSCNDCPKETVPSMETGLCA 366
Qy 540 DTAFTPKSELCREBEPTSDTCGFTFRPGAFPTNYSYTDNCTDNFTPNQVARNHCYLDL 599
Db 367 DTAFTPKSELCREBEPTSDTCGFTFRPGAFPTNYSYTDNCTDNFTPNQVARNHCYLDL 426
Qy 600 VTQQMTSRKPTPIPIPPMVIIGQTNKSLTIHMLPRISGVYVYDASGSLGCACTEDGFRQ 659
Db 427 VTQQMTSRKPTPIPIPPMVIIGQTNKSLTIHMLPRISGVYVYDASGSLGCACTEDGFRQ 486
Qy 660 YHHTASSRRVCDSSGYMTPEEAVGPVPVDPCEPSLOAMSEVHLVYMNMTVPCEPTGCS 719
Db 487 YHHTASSRRVCDSSGYMTPEEAVGPVPVDPCEPSLOAMSEVHLVYMNMTVPCEPTGCS 546
Qy 720 LELLFQHPVQADTLTLVWTSFFMSSQVLPDTEILLENKESVHLGPDTECDIPLTIKLH 779
Db 547 LELLFQHPVQADTLTLVWTSFFMSSQVLPDTEILLENKESVHLGPDTECDIPLTIKLH 606
Qy 780 VDGKVSQVQYTYTDERIEIDAALLTSQPSHPLCSGCPVRYQVLRDPPFASGLPVVYTHS 839
Db 607 VDGKVSQVQYTYTDERIEIDAALLTSQPSHPLCSGCPVRYQVLRDPPFASGLPVVYTHS 666
Qy 840 HRKFTDVEVTGQMYQYVLAAGGELGSEASPLNHIHGA PYCGDKYSERLGECCDDG 899
Db 667 HRKFTDVEVTGQMYQYVLAAGGELGSEASPLNHIHGA PYCGDKYSERLGECCDDG 726
Qy 900 LVSQDGSKYCELEBGFNCVGEPSLCYMEGDGICEPFRKTSIYDCGIYTPKGYLDQW 959
Db 727 LVSQDGSKYCELEBGFNCVGEPSLCYMEGDGICEPFRKTSIYDCGIYTPKGYLDQW 786
Qy 960 TRAYSHHEKXKCPVSLVYGEBSHLSICTSYHPDLPHNRPLTGMPCVASENTOODRSQ 1019
Db 787 TRAYSHHEKXKCPVSLVYGEBSHLSICTSYHPDLPHNRPLTGMPCVASENTOODRSQ 846
Qy 1020 PEGSLKKEDEBVMKVCENRPGEARAIFILTTDGLVGEHQOPTYTLVLTVDVRSNHSIG 1079
Db 847 PEGSLKKEDEBVMKVCENRPGEARAIFILTTDGLVGEHQOPTYTLVLTVDVRSNHSIG 906
Qy 1080 TYGLSCQHNPLIINTVTHQNVLFHHTTSYLVNFPSSPRVGISAVALTSSRIGLSAPNSCI 1139
Db 907 TYGLSCQHNPLIINTVTHQNVLFHHTTSYLVNFPSSPRVGISAVALTSSRIGLSAPNSCI 966
Qy 1140 SEDEGQNHQGSCHIRPCGKQDCPSLLLDHADVNCISIGPLMKCAITTCQGFALQAS 1199
Db 967 SEDEGQNHQGSCHIRPCGKQDCPSLLLDHADVNCISIGPLMKCAITTCQGFALQAS 1026
Qy 1200 SGOYIRPMQKEIILTCSSGHDQNVSCLPVDCGVPDPSLVNYANFSCSEBGTFLKRCISIS 1259
Db 1027 SGOYIRPMQKEIILTCSSGHDQNVSCLPVDCGVPDPSLVNYANFSCSEBGTFLKRCISIS 1086
Qy 1260 CVPRAKLGSLPWLTCLEEDGLMSLPEVYCKLECDAPPIILNANLLPHCLQDNHVDGTTIC 1319
Db 1087 CVPRAKLGSLPWLTCLEEDGLMSLPEVYCKLECDAPPIILNANLLPHCLQDNHVDGTTIC 1146
Qy 1320 KYECKPGYVAASABSKVANKLKIQCLEGGIMEGSSCIPVCEPPRPVEBAMECTGNGF 1379
Db 1147 KYECKPGYVAASABSKVANKLKIQCLEGGIMEGSSCIPVCEPPRPVEBAMECTGNGF 1206
Qy 1380 SLDSQCVLNCQREKLPILCTKEGLMTQEFKLCENLQGECPRPPELSNVEYKCEQGYG 1439
Db 1207 SLDSQCVLNCQREKLPILCTKEGLMTQEFKLCENLQGECPRPPELSNVEYKCEQGYG 1266
Qy 1440 IGAVCSPLCVIIPSPDPMLENITADTLEHMEPVKVQSIYCTGRQWHPDVLVHCIOQC 1499
Db 1267 IGAVCSPLCVIIPSPDPMLENITADTLEHMEPVKVQSIYCTGRQWHPDVLVHCIOQC 1326
Qy 1500 CEPFOADGWKDTINRNYCHYDGDCCSSTLSKVIIPPAADCLDECTCDPRAENQ 1558

Db 1327 CEPQADGWCDDTINNRAVCHYDGDCCSSTLSKKVIFPAADCDLDECTCRDPAEENQ 1385

RESULT 7

US-10-675-685-16

/ Sequence 16, Application US/10675685

/ Publication No. US20040063134A1

/ GENERAL INFORMATION:

/ APPLICANT: Gu, Yizhong

/ APPLICANT: Shannon, Mark

/ TITLE OF INVENTION: NOVEL ISOFORMS OF HUMAN PREGNANCY-ASSOCIATED PROTEIN E

/ FILE REFERENCE: PB0114

/ CURRENT APPLICATION NUMBER: US/10/675.685

/ CURRENT FILING DATE: 2003-09-30

/ PRIOR APPLICATION NUMBER: US 60/207,456

/ PRIOR FILING DATE: 2000-05-26

/ PRIOR APPLICATION NUMBER: US 60/236,359

/ PRIOR FILING DATE: 2000-09-27

/ NUMBER OF SEQ ID NOS: 1881

/ SOFTWARE: Aecomica Sequence Listing Engine

/ SEQ ID NO 16

/ LENGTH: 1385

/ TYPE: PRT

/ ORGANISM: Homo sapiens

US-10-675-685-16

Query Match 36.8%; Score 574; DB 15; Length 1385;

Best Local Similarity 99.5%; Pred. No. 0;

Matches 1074; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

Qy 480 GGIYLSPAYYGMPGHTDTHIHVGHVGLVHVPKGVSRSSCNDPCKETVPSMETGDLCA 539

Db 307 GGIYLSPAYYGMPGHTDTHIHVGHVGLVHVPKGVSRSSCNDPCKETVPSMETGDLCA 366

Qy 540 DTATPKSELCREBEPTSDTCGTRPGAPPTNMYSTDDCTNFTPNQVARMHCYIDL 599

Db 367 DTATPKSELCREBEPTSDTCGTRPGAPPTNMYSTDDCTNFTPNQVARMHCYIDL 426

Qy 600 VYQWTSRKPTPIPIPMVIGQNKSLTIHMLPPIGIVYDRAAGSLCGACTEDGTFRQ 659

Db 427 VYQWTSRKPTPIPIPMVIGQNKSLTIHMLPPIGIVYDRAAGSLCGACTEDGTFRQ 486

Qy 660 YVHTASRRVCDSSGYMTPREAVGPVVDQCEPSLQAMSEVLYHMMNTVPCPTGCS 719

Db 487 YVHTASRRVCDSSGYMTPREAVGPVVDQCEPSLQAMSEVLYHMMNTVPCPTGCS 546

Qy 720 LELLFQHPVQADTTLVWTSFFMSSQVLPFTTEILENKESVHLGPIIDTFCDIPLITKLH 779

Db 547 LELLFQHPVQADTTLVWTSFFMSSQVLPFTTEILENKESVHLGPIIDTFCDIPLITKLH 606

Qy 780 VDGKVSQVYVTFDERIEIDALLTSQPHSPLCSGCRPVRYQVLRDPPFASGLPVVYTHS 839

Db 607 VDGKVSQVYVTFDERIEIDALLTSQPHSPLCSGCRPVRYQVLRDPPFASGLPVVYTHS 666

Qy 840 HRKRTDEVYTPGQVYQVYLAAGGELGASPLNHNHIGAPYCGDKVSESLGECDDGD 899

Db 667 HRKRTDEVYTPGQVYQVYLAAGGELGASPLNHNHIGAPYCGDKVSESLGECDDGD 726

Qy 900 LVSGDGSKVCLEEGFCVSGEPLCYMYEGDGI CEPPERSTSLVDGITYPKYLDOMA 959

Db 727 LVSGDGSKVCLEEGFCVSGEPLCYMYEGDGI CEPPERSTSLVDGITYPKYLDOMA 786

Qy 960 TRAVSSHEDKKKCVSLVTGEPHSLICTSYNPDLPNHRPLTGMPFCVASENETODDSEQ 1019

Db 787 TRAVSSHEDKKKCVSLVTGEPHSLICTSYNPDLPNHRPLTGMPFCVASENETODDSEQ 846

Qy 1020 PEGSLKKEDEWMLKVCPRRBEARALIFLITTDGLVGEHQOFTVTLVTVRSNHSLG 1079

Db 847 PEGSLKKEDEWMLKVCPRRBEARALIFLITTDGLVGEHQOFTVTLVTVRSNHSLG 906

Qy 1080 TYGSCQHNPLIINVTHHQNVLPHHTTSVLNFSPPRGISAVVALRTSSRIGLSAPSNCI 1139

Db 907 TYGSCQHNPLIINVTHHQNVLPHHTTSVLNFSPPRGISAVVALRTSSRIGLSAPSNCI 966

Qy 1140 SEDEGQNHOGQSCIHRCQKQDSCPSLLLDHADVNTCTSIGPGLMKCAITCORGFALQAS 1199

Db 967 SEDEGQNHOGQSCIHRCQKQDSCPSLLLDHADVNTCTSIGPGLMKCAITCORGFALQAS 1026

Qy 1200 SGOYIRPMQREILLTCSSGHMDQNVSCLPVDCGVPDPSLVNRYANFSCBSGTFKLKRCIS 1259

Db 1027 SEGYIRLMQREILLTCSSGHMDQNVSCLPVDCGVPDPSLVNRYANFSCBSGTFKLKRCIS 1086

Qy 1260 CVPPAKIQGISPMWLTCLDEGLMSLPEVYCYLCECDAPPIIINANILLPHCLDNDHVDGTC 1319

Db 1087 CVPPAKIQGISPMWLTCLDEGLMSLPEVYCYLCECDAPPIIINANILLPHCLDNDHVDGTC 1146

Qy 1320 KYECKPGYVAESAEGVARNKLLKIQCLBGIWQSGCIPVYCEPPVPEGMECTNGF 1379

Db 1147 KYECKPGYVAESAEGVARNKLLKIQCLBGIWQSGCIPVYCEPPVPEGMECTNGF 1206

Qy 1380 SLDSQCVLANQREKRLPICTKEGLWTOEFKLCENIQGBCPPPSSELSNVEYKCEQGYG 1439

Db 1207 SLDSQCVLANQREKRLPICTKEGLWTOEFKLCENIQGBCPPPSSELSNVEYKCEQGYG 1266

Qy 1440 IGAVCSPLCVIPSDPVMLEPNITADTLEHMMBEPKVQSI VCTGRQWHPDPVLVHCIOG 1499

Db 1267 IGAVCSPLCVIPSDPVMLEPNITADTLEHMMBEPKVQSI VCTGRQWHPDPVLVHCIOG 1326

Qy 1500 CEPQADGWCDDTINNRAVCHYDGDCCSSTLSKKVIFPAADCDLDECTCRDPAEENQ 1558

Db 1327 CEPQADGWCDDTINNRAVCHYDGDCCSSTLSKKVIFPAADCDLDECTCRDPAEENQ 1385

RESULT 8

US-09-664-761-34265

/ Sequence 34265, Application US/09864761

/ Patent No. US20020048763A1

/ GENERAL INFORMATION:

/ APPLICANT: Penn, Sharon G.

/ APPLICANT: Rank, David R.

/ APPLICANT: Hanzel, David K.

/ APPLICANT: Chen, Wenheng

/ TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR

/ FILE REFERENCE: Aecomica-X-1

/ CURRENT APPLICATION NUMBER: US/09/664.761

/ CURRENT FILING DATE: 2001-05-23

/ PRIOR APPLICATION NUMBER: US 60/180,312

/ PRIOR FILING DATE: 2000-02-04

/ PRIOR APPLICATION NUMBER: US 60/207,456

/ PRIOR FILING DATE: 2000-05-26

/ PRIOR APPLICATION NUMBER: US 09/632,366

/ PRIOR FILING DATE: 2000-08-03

/ PRIOR APPLICATION NUMBER: GB 24263.6

/ PRIOR FILING DATE: 2000-10-04

/ PRIOR APPLICATION NUMBER: US 60/236,359

/ PRIOR FILING DATE: 2000-09-27

/ PRIOR APPLICATION NUMBER: PCT/US01/00666

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00667

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00664

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00669

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00665

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00668

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00663

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00662

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00661

/ PRIOR FILING DATE: 2001-01-30

/ PRIOR APPLICATION NUMBER: PCT/US01/00670


```

PRIORITY FILING DATE: 2001-01-30
PRIORITY APPLICATION NUMBER: US 60/234,687
PRIORITY FILING DATE: 2000-09-21
PRIORITY APPLICATION NUMBER: US 09/608,408
PRIORITY FILING DATE: 2000-06-30
PRIORITY APPLICATION NUMBER: US 09/774,203
PRIORITY FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
SOFTWARE: Anomax Sequence Listing Engine vers. 1.1
SEQ ID NO 34265
LENGTH: 192
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
OTHER INFORMATION: MAP TO A1031734.9
OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 44
OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 1.1
OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6
OTHER INFORMATION: EST HUMAN HIT: A0140701.1, EVALU 2.00e-53
OTHER INFORMATION: SWISSPROT HIT: P07207, EVALU 3.00e-04
US-09-864-761-34265

```

Query Match	12.3%	Score 192	DB 9	Length 192
Best Local Similarity	100.0%	Pred. No.	1.2e-160	
Matches 192; Conservative	0	Mismatches	0	Gaps 0

Qy	239	DEKXPRLEVLQGEPEPELLSPLOPPLCGQYICDNVELISQYNGWPLRGKXTRYOVN	238
Db	1	DEKXPRLEVLQGEPEPELLSPLOPPLCGQYICDNVELISQYNGWPLRGKXTRYOVN	60
Qy	299	ICDDEGNLPVSEEOQLRQHEALNEAFSRYNYSWQLSHYOHNSTLRHVVLYNCEESKI	356
Db	61	ICDDEGNLPVSEEOQLRQHEALNEAFSRYNYSWQLSHYOHNSTLRHVVLYNCEESKI	120
Qy	359	GNDHCDPECEHPLTYGDGDGDCRLQRCYCSWMNRDGLCHVECNMMLNDFDDGCCDPOVAD	418
Db	121	GNDHCDPECEHPLTYGDGDGDCRLQRCYCSWMNRDGLCHVECNMMLNDFDDGCCDPOVAD	180
Qy	419	VKTKCEPDSPK	430
Db	181	VKTKCEPDSPK	192

RESULT 9
 US-09-864-761-34264
 ; Sequence 34264, Application US/09864761
 ; Patent No. US20020048763A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Penn, Sharon G.
 ; APPLICANT: Rank, David R.
 ; APPLICANT: Hanzel, David K.
 ; APPLICANT: Chen, Wensheng
 ; TITLE OF INVENTION: HUMAN BSNOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
 ; FILE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
 ; FILE REFERENCE: Aecm1ca-X-1
 ; CURRENT APPLICATION NUMBER: US/09/864,761
 ; CURRENT FILING DATE: 2001-05-23
 ; PRIOR APPLICATION NUMBER: US 60/180,312
 ; PRIOR FILING DATE: 2000-02-04
 ; PRIOR APPLICATION NUMBER: US 60/207,456
 ; PRIOR FILING DATE: 2000-05-26
 ; PRIOR APPLICATION NUMBER: US 09/632,366
 ; PRIOR FILING DATE: 2000-08-03
 ; PRIOR APPLICATION NUMBER: GB 24263.6
 ; PRIOR FILING DATE: 2000-10-04
 ; PRIOR APPLICATION NUMBER: US 60/236,359

```

1      PRIOR FILING DATE: 2000-09-27
2      PRIOR APPLICATION NUMBER: PCT/US01/00666
3      PRIOR FILING DATE: 2001-01-30
4      PRIOR APPLICATION NUMBER: PCT/US01/00667
5      PRIOR FILING DATE: 2001-01-30
6      PRIOR APPLICATION NUMBER: PCT/US01/00664
7      PRIOR FILING DATE: 2001-01-30
8      PRIOR APPLICATION NUMBER: PCT/US01/00669
9      PRIOR FILING DATE: 2001-01-30
10     PRIOR APPLICATION NUMBER: PCT/US01/00665
11     PRIOR FILING DATE: 2001-01-30
12     PRIOR APPLICATION NUMBER: PCT/US01/00668
13     PRIOR FILING DATE: 2001-01-30
14     PRIOR APPLICATION NUMBER: PCT/US01/00663
15     PRIOR FILING DATE: 2001-01-30
16     PRIOR APPLICATION NUMBER: PCT/US01/00662
17     PRIOR FILING DATE: 2001-01-30
18     PRIOR APPLICATION NUMBER: PCT/US01/00661
19     PRIOR FILING DATE: 2001-01-30
20     PRIOR APPLICATION NUMBER: PCT/US01/00670
21     PRIOR FILING DATE: 2001-01-30
22     PRIOR APPLICATION NUMBER: US 60/234,687
23     PRIOR FILING DATE: 2000-09-21
24     PRIOR APPLICATION NUMBER: US 09/608,408
25     PRIOR FILING DATE: 2000-06-30
26     PRIOR APPLICATION NUMBER: US 09/774,203
27     PRIOR FILING DATE: 2001-01-29
28     NUMBER OF SEQ ID NOS: 49117
29
30     SOFTWARE: Annonmax Sequence Listing Engine vers. 1.1.1
31     SEQ ID NO 34264

```

```

1  TYPE: PRT
2  ORGANISM: Homo sapiens
3  FEATURE:
4  OTHER INFORMATION: MAP TO AL031734.9
5  OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 1.6
6  OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 1.3
7  OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 44
8  OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 1.6
9  OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 1.8
10 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 1.4
11 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1.9
12 OTHER INFORMATION: EXPRESSED IN HEL100, SIGNAL = 1.1
13 OTHER INFORMATION: EXPRESSED IN HEAT1, SIGNAL = 1.1
14 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 4.6
15 OTHER INFORMATION: SWISSPROT HIT: P28977, EVALU1 1.60e+00
16 OTHER INFORMATION: EST_HUMAN HIT: BF366974.1, EVALU0 4.00e-36
17 JS-09-864-761-34264

```

```

Query Match      4.5%; Score 70; DB 9; Length 70;
Best Local Similarity 100.0%; Pred. No. 2.le-60;
Matches 70; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY           75 VEDNCSHIVSDKGWALGIRSGKDKGRDARFFPSLCTDRVKKATILISHSRYPGTWTHTV 134
              |||||||
Db            1 VFDSNSHVSDKGWALGIRSGKDKGRDARFFPSLCTDRVKKATILISHSRYPGTWTHTV 60

QY           135 AATYDGRHMA 144
              |||||
Db            61 AATYDGRHMA 70

RESULT 10
US-09-864-761-34262
; Sequence 34262, Application US/09864761
; Patent No. US20020048763A1
; GENERAL INFORMATION:
;; APPLICANT: Penn, Sharon G.
;; APPLICANT: Rank, David R.
;; APPLICANT: Hanzel, David K.
;; APPLICANT: Chen, Wensheng
;; TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FOR
;; TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY
```


FILE REFERENCE: Aecomica-X-1
 CURRENT APPLICATION NUMBER: US/09/864,761
 PRIOR FILING DATE: 2001-05-23
 PRIOR APPLICATION NUMBER: US 60/180,312
 PRIOR FILING DATE: 2000-02-04
 PRIOR APPLICATION NUMBER: US 60/207,456
 PRIOR FILING DATE: 2000-05-26
 PRIOR APPLICATION NUMBER: US 09/632,366
 PRIOR FILING DATE: 2000-08-03
 PRIOR APPLICATION NUMBER: GB 24263,6
 PRIOR FILING DATE: 2000-10-04
 PRIOR APPLICATION NUMBER: US 60/236,359
 PRIOR FILING DATE: 2000-09-27
 PRIOR APPLICATION NUMBER: PCT/US01/00666
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00667
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00664
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00669
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00665
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00668
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00663
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00662
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00661
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: PCT/US01/00670
 PRIOR FILING DATE: 2001-01-30
 PRIOR APPLICATION NUMBER: US 60/234,687
 PRIOR FILING DATE: 2000-09-21
 PRIOR APPLICATION NUMBER: US 09/608,408
 PRIOR FILING DATE: 2000-06-30
 PRIOR APPLICATION NUMBER: US 09/774,203
 PRIOR FILING DATE: 2001-01-29
 NUMBER OF SEQ ID NOS: 49117
 SOFTWARE: Annomax Sequence Listing Engine vers. 1.1
 SEQ ID NO 34262
 LENGTH: 63
 TYPE: PRT
 ORGANISM: Homo sapiens
 FEATURE:
 OTHER INFORMATION: MAP TO AL031734.9
 OTHER INFORMATION: EXPRESSED IN HBL100, SIGNAL = 0.87
 OTHER INFORMATION: EXPRESSED IN PLACENTA, SIGNAL = 74
 OTHER INFORMATION: EXPRESSED IN BT474, SIGNAL = 0.84
 OTHER INFORMATION: EXPRESSED IN BONE MARROW, SIGNAL = 1
 OTHER INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 0.82
 OTHER INFORMATION: EXPRESSED IN LUNG, SIGNAL = 0.9
 OTHER INFORMATION: EXPRESSED IN HELA, SIGNAL = 0.89
 OTHER INFORMATION: EXPRESSED IN ADULT LIVER, SIGNAL = 0.8
 OTHER INFORMATION: EXPRESSED IN BRAIN, SIGNAL = 0.79
 OTHER INFORMATION: EXPRESSED IN HEART, SIGNAL = 1
 OTHER INFORMATION: EST_HUMAN HIT: A1075970.1, EVALUATE 7.00e-03
 US-09-864-761-34262

Query Match 4.0%; Score 63; DB 9; Length 63;
 Best Local Similarity 100.0%; Pred. No. 1.6e-53;
 Matches 63; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 11 GEGSVREATNSQVGLPILYFSGRRRLLRPEVLAIRPEAFVTEAMVPEGGONNPA 70
 Db 1 GEGSVREATNSQVGLPILYFSGRRRLLRPEVLAIRPEAFVTEAMVPEGGONNPA 60
 Oy 71 IIA 73
 Db 61 IIA 63

RESULT 11
 US-10-741-600-1402
 Sequence 1402, Application US/10741600
 Publication No. US20050026169A1
 GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CU001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1402
 LENGTH: 704
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-741-600-1402

Query Match 1.2%; Score 18; DB 17; Length 704;
 Best Local Similarity 100.0%; Pred. No. 4.4e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 585 FTPNQVARMHCYLDLVYQ 602
 Db 440 FTPNQVARMHCYLDLVYQ 457

RESULT 12
 US-10-334-143-85
 Sequence 85, Application US/10334143
 Publication No. US20040009549A1
 GENERAL INFORMATION:
 APPLICANT: GRIGORIEV, IGOR VYACHESLAVOVICH
 APPLICANT: SUDARSANAM, SUCHA
 TITLE OF INVENTION: METHOD FOR DETECTING REMOTE HOMOLOGUES AND NOVEL KINASES IDENTIFIED WITH THE METHOD
 FILE REFERENCE: 038602/1543
 CURRENT APPLICATION NUMBER: US/10/334,143
 CURRENT FILING DATE: 2002-12-31
 PRIOR APPLICATION NUMBER: 60/343,169
 PRIOR FILING DATE: 2001-12-31
 NUMBER OF SEQ ID NOS: 207
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 85
 LENGTH: 858
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-10-334-143-85

Query Match 1.2%; Score 18; DB 15; Length 858;
 Best Local Similarity 100.0%; Pred. No. 5.3e-08;
 Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Oy 585 FTPNQVARMHCYLDLVYQ 602
 Db 594 FTPNQVARMHCYLDLVYQ 611

RESULT 13
 US-10-741-600-1404
 Sequence 1404, Application US/10741600
 Publication No. US20050026169A1
 GENERAL INFORMATION:
 APPLICANT: CARGILL, Michele et al.
 TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH MYOCARDIAL INFARCTION, METHODS OF DETECTION AND USES THEREOF
 FILE REFERENCE: CU001499
 CURRENT APPLICATION NUMBER: US/10/741,600
 CURRENT FILING DATE: 2003-12-22
 NUMBER OF SEQ ID NOS: 73997
 SOFTWARE: FastSeq for Windows Version 4.0
 SEQ ID NO 1404

```

; LENGTH: 1232
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1404

```

```

Query Match          1.2%; Score 18; DB 17; Length 1232;
Best Local Similarity 100.0%; Pred. No. 7.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      585 FTPNQVARMHCYLDLVYQ 602
      |||||||
Db      440 FTPNQVARMHCYLDLVYQ 457

```

```

RESULT 14
US-10-741-600-1403
; Sequence 1403, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1403
; LENGTH: 1420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1403

```

```

Query Match          1.2%; Score 18; DB 17; Length 1420;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      585 FTPNQVARMHCYLDLVYQ 602
      |||||||
Db      440 FTPNQVARMHCYLDLVYQ 457

```

```

RESULT 15
US-10-741-600-1405
; Sequence 1405, Application US/10741600
; Publication No. US20050026169A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; FILE REFERENCE: CLO01499
; CURRENT APPLICATION NUMBER: US/10/741,600
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 73997
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1405
; LENGTH: 1420
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-741-600-1405

```

```

Query Match          1.2%; Score 18; DB 17; Length 1420;
Best Local Similarity 100.0%; Pred. No. 8.3e-08;
Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

```

```

OY      585 FTPNQVARMHCYLDLVYQ 602
      |||||||
Db      440 FTPNQVARMHCYLDLVYQ 457

```

Search completed: August 25, 2005, 22:32:01
 Job time : 120 secs